

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 20, 2004, 08:42:51 ; Search time 1988 Seconds

(without alignments)
585.827 Million cell updates/sec

Title: US-09-435-471b-9

Perfect score: 39
Sequence: 1 taactctgaattttaaaccggaagtcagagctagta 39

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 203984

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

EST:
1: em_estba:*
2: em_estchum:*
3: em_estcin:*
4: em_estcmu:*
5: em_estcov:*
6: em_estcpl:*
7: em_estcro:*
8: em_estc1:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estlum:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrt1:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	17.8	45.6	46	9	AA875851	OB34C05.S
2	17.4	44.6	56	29	CU002662	CU002662.02S0169.0
3	17.2	44.1	50	28	B2765559	B2765559.SALK.1316
4	17	43.6	56	28	B02877	B02877.CSRL-161G3-

C 5	16.8	43.1	45	28	B2766643	B2766643.SALK.1376
C 6	16.6	42.6	51	13	B0625561	B0625561.rdi7C06.Y
C 7	16.6	42.6	54	29	DM6545095	DM6545095.Drosophila
C 8	16.4	42.1	53	29	CU002273	CU002273.02S0105-0
C 9	16.4	42.1	60	28	B2665081	B2665081.SALK.1106
C 10	16.2	41.5	55	28	B2667225	B2667225.SALK.0262
C 11	16.2	41.5	57	14	CA334810	CA334810.NISC.1E01
C 12	16.1	41.0	50	9	AU106257	AU106257.AU106257
C 13	15.8	40.5	51	13	B0786274	B0786274.sag65H01.
C 14	15.8	40.5	52	9	AA531325	AA531325.n515G04.S
C 15	15.8	40.5	59	14	W38942	W38942.ZB28C08.r1
C 16	15.6	40.0	34	28	B2764154	B2764154.SALK.1240
C 17	15.6	40.0	34	28	B2764155	B2764155.SALK.1240
C 18	15.6	40.0	56	10	AW510712	AW510712.hd36e09.x
C 19	15.4	39.5	60	28	B2761908	B2761908.SALK.0830
C 20	15.2	39.0	37	28	BH791558	BH791558.SALK.0604
C 21	15.2	39.0	55	28	AZ5314607	AZ5314607.1M0361K23
C 22	15.2	39.0	57	28	AZ531462	AZ531462.AST-2E046
C 23	15.2	39.0	60	13	BQ785544	BQ785544.sag79e10.
C 24	15	38.5	36	29	BX656784	BX656784.Arabidops
C 25	15	38.5	45	10	BE896253	BE896253.601438976
C 26	15	38.5	54	12	B1865787	B1865787.f127e04.x
C 27	15	38.5	58	29	AL952767	AL952767.Arabidops
C 28	15	38.5	59	9	AF090227	AF090227.AF090227
C 29	15	38.5	59	9	AV561680	AV561680.AV561680
C 30	15	38.5	60	14	CF330014	CF330014.NACL--05-
C 31	14.8	37.9	45	28	AZ812554	AZ812554.2M0079K15
C 32	14.8	37.9	45	28	B2290823	B2290823.SALK.0915
C 33	14.8	37.9	52	10	BP647818	BP647818.NP012D01E
C 34	14.8	37.9	58	9	AV969325	AV969325.AV969325
C 35	14.8	37.9	59	12	BG361064	BG361064.gd45d09.Y
C 36	14.6	37.4	39	28	AZ312103	AZ312103.1M0041G24
C 37	14.6	37.4	46	9	AU256186	AU256186.AU256186
C 38	14.6	37.4	50	28	BH906653	BH906653.SALK.0351
C 39	14.6	37.4	51	14	CB058336	CB058336.NISC.1K03
C 40	14.6	37.4	52	9	AA170232	AA170232.ms80G10.r
C 41	14.6	37.4	53	28	AZ488804	AZ488804.1M0319H15
C 42	14.6	37.4	60	9	AA554929	AA554929.nk31G05.S
C 43	14.6	37.4	60	12	BG271466	BG271466.na157d04.
C 44	14.6	37.4	60	12	BG271507	BG271507.na158d05.
C 45	14.6	37.4	60	12	BG370294	BG370294.na129h04.

ALIGNMENTS

RESULT 1
AA875851/C
LOCUS
DEFINITION
OB34C05.81 NCI-CGAP Kids Homo sapiens cDNA clone IMAGE:1325576 3'
similar to SW:AF11_HUMAN P55008 ALLOGRAFT INFLAMMATORY FACTOR-1 ;
mRNA sequence.
ACCESSION
AA875851
VERSION
AA875851.1 GI:2985210
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 (bases 1 to 46)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TUMOR
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Unpublished (1997)
JOURNAL
Contact: Robert Strausberg, Ph.D.
COMMENT
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LMN at:

www-bio.lnl.gov/bdrrp/image/image.html
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers

FEATURES

source

1. .46
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1325576"
/tissue_type="2 pooled tumors (clear cell type)"
/lab_host="DH10B"
/clone_1ib="NCI CGAP Kids"
/note="Organ: kidney; Vector: pT73D-Pac (pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer 15' AACTGGAAGATTCGGCGCCGCAATATTTTATTTTATTTT 3', double-stranded cDNA was ligated to Eco RI adaptors (pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 45.6%; Score 17.8; DB 9; Length 46;
Best Local Similarity 75.9%; Pred. No. 1.5e+04;
Matches 22; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 5 TCTGAATTTTAAACCCGAGTCACAG 33
Db 39 TCGGAATTTTAAAGCCCAAGGAACAG 11

RESULT 2
CL002662/c 56 bp DNA linear GSS 19-DEC-2003
LOCUS 02S0169-07A1-G05 UniformMu MutAlt Library Zea mays genomic clone
DEFINITION 02S0169-07A1-G05, genomic survey sequence.
ACCESSION CL002662
VERSION CL002662.1 GI:40219741
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
REFERENCE 1 (bases 1 to 56)
AUTHORS Latshaw,S., Tan,B.-C., Settles,A.M. and McCarty,D.R.
TITLE Sequence tagged transposon insertions from the UniformMu maize population
JOURNAL Unpublished (2003)
COMMENT Contact: Donald R. McCarty
Plant Molecular and Cellular Biology Program
University of Florida
PO 110690 Gainesville, FL 32611-0690, USA
Tel: 352-392-1928 x322
Email: drmc@ufl.edu
Sequence flanking probable Mu insertion site in UniformMu line:
02S0169-07, Primer set: A
Class: transposon insertion site.

FEATURES

source

1. .56
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="W22 (ACR, bz1-m9)"
/cultivar="UniformMu"
/db_xref="taxon:4577"
/clone="02S0169-07A1-G05"
/note="Vector: TOPO-PCR4; DNA flanking Mu transposon insertions in Mu inactive lines were extracted from the UniformMu maize population by the thermo asymmetric interlaced PCR (TAIL) protocol using primers specific for the Mu terminal inverted repeat and a set of 16 arbitrary

ORIGIN

Query Match 44.1%; Score 17.4; DB 29; Length 56;
Best Local Similarity 77.8%; Pred. No. 2.2e+04;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5 TCTGAATTTTAAACCCGAGTCACAG 31
Db 55 TCGGAATTTCTGAACCTAGTAAAG 29

RESULT 3
BZ765559/c 50 bp DNA linear GSS 13-MAR-2003
LOCUS SALK_131696.45.85.x Arabidopsis thaliana TDNA insertion lines
DEFINITION Arabidopsis thaliana genomic clone SALK_131696.45.85.x, genomic survey sequence.

ACCESSION BZ765559
VERSION BZ765559.1 GI:28938112
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 50)
AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shim,P., Zimmermann,J. and Ecker,J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
JOURNAL Unpublished (2001)
COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGAL)
Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of TDNA.
Class: TDNA tagged.

FEATURES

source

Location/Qualifiers
1. .50
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_131696.45.85.x"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/cdna_protocols.html

ORIGIN

Query Match 44.1%; Score 17.2; DB 28; Length 50;
Best Local Similarity 65.8%; Pred. No. 2.6e+04;
Matches 25; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 2 AACTGGAATTTTAAACCCGAGTCACAGCTAGTA 39
Db 50 AATTGGAATTTGTTAAACTTAAGTAAAGGAATA 13

RESULT 4
B02877/c 56 bp DNA linear GSS 13-JUL-1996
LOCUS B02877
DEFINITION CSRL-161G3-u CSRL flow sorted Chromosome 11 specific cosmid Homo

sapiens genomic clone cSRL-161G3, genomic survey sequence.
 B02877
 VERSION B02877.1 GI:1412155
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 56)
 REFERENCE Evans, G.A., Burbee, D., Davies, C., Hahner, L., Oliver, T., Gilbert, M., Jones, D., Ward, T., Gillian, E., Schagemann, J., Probst, S., Harris, J., Depord, J., McFarland, J., Butzinski, K., Khan, M., Kupfer, K., and Garner, H.R.
 Genomic Sequence Sampled Map of Chromosome 11
 Unpublished (1996)
 CONTACT Contact: Evans GA, Shane Probst
 Dermott Center for Human Growth and Development
 University of Texas Southwestern Medical Center At Dallas
 5323 Harry Hines Blvd, Dallas TX 75235-8591
 Tel: 214-648-1600
 Fax: 214-648-1666
 Email: gevas@utsw.swmed.edu, shane@dermott.swmed.edu
 Seq primer: T7
 Class: cosmid ends
 High quality sequence stop: 56.
 Location/Qualifiers
 1..56
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone="cSRL-161G3"
 /sex="female"
 /cell_type="chimeric hamster somatic cell hybrid"
 /clone_lib="cSRL Flow sorted Chromosome 11 specific cosmid"
 /note="Vector: SCOS-1; Human Chromosome 11 specific cosmid library prepared from flow sorted human Chromosome 11 derived from Chinese Hamster Ovary (CHO) monochromosomal somatic cell hybrid, J1"

ORIGIN
 Query Match 43.6%; Score 17; DB 28; Length 56;
 Best Local Similarity 76.9%; Pred. No. 3.2e+04;
 Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 AACTCGAATTTTAAACCCGAGT 27
 43 AATTTGTTTAAACCGAAT 18

RESULT 5
 B2766643/c 45 bp DNA linear GSS 13-MAR-2003
 LOCUS SALK_137659.19.20.x Arabidopsis thaliana TDNA insertion lines
 DEFINITION Arabidopsis thaliana genomic clone SALK_137659.19.20.x, genomic survey sequence.
 ACCESSION B2766643
 VERSION B2766643.1 GI:28939196
 KEYWORDS GSS.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliopsida; euclidyales; core euclids; rosids; eustosida II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 45)
 REFERENCE Alonso, J.M., Leisner, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J., and Ecker, J.R.
 A Sequence-indexed library of Insertion Mutations in the Arabidopsis Genome
 Unpublished (2001)
 CONTACT Contact: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGAL)

The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salk.edu
 This is single pass sequence recovered from the left border of TDNA.
 Class: TDNA tagged.
 Location/Qualifiers
 1..45
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone="SALK_137659.19.20.x"
 /clone_lib="Arabidopsis thaliana TDNA insertion lines"
 /note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html

ORIGIN
 Query Match 43.1%; Score 16.8; DB 28; Length 45;
 Best Local Similarity 75.0%; Pred. No. 3.8e+04;
 Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 7 TGAATTTTAAACCCGAGTCAAGAC 34
 44 TGAATCATTAACCAAGTCAAGTC 17

RESULT 6
 B0625561/c 51 bp mRNA linear EST 01-JUL-2002
 LOCUS rd17606.y1 Meloidogyne incognita egg S11 TOPO v1 Meloidogyne incognita cDNA 5', mRNA sequence.
 DEFINITION B0625561
 ACCESSION B0625561.1 GI:21652739
 VERSION B0625561
 KEYWORDS EST.
 SOURCE Meloidogyne incognita (southern root-knot nematode)
 ORGANISM Meloidogyne incognita
 Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina; Tylenchoidea; Heterodridae; Meloidogyninae; Meloidogyne.
 1 (bases 1 to 51)

REFERENCE McCarter, J., Clifton, S., Chapell, B., Pape, D., Martin, J., Wylie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B., Bowers, Y., Gibbons, M., Ralber, E., Bennett, J., Franklin, C., Tsagaris, H., Ronko, I., Kennedy, S., Maguire, L., Beck, C., Underwood, K., Steptoe, M., Allen, M., Persson, B., Swaller, T., Harvey, N., Schurk, R., Kohn, S., Shih, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R., and Wilson, R.
 The Washington Univ. Nematode EST Project, 1999
 Unpublished (1999)
 CONTACT Contact: McCarter JP
 The Washington Univ. Nematode EST Project, 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.edu

The library was constructed by Claire Murphy and Dr. James McCarter at Washington University, St. Louis. Meloidogyne incognita eggs were provided by Andrew Klock of Divergence Inc., St. Louis, MO. Putative full length read
 The vector to vector length is 52
 Seq primer: -40RP from Gibco.

FEATURES
 source
 1..51
 /organism="Meloidogyne incognita"
 /mol_type="mRNA"
 /db_xref="taxon:6306"

/dev stage="egg"
 /lab_host="DH10B (Invitrogen)"
 /clone_lib="Meloidogyne incognita egg SL1 TOPO v1"
 /note="Vector: pCRII-TOPO (Invitrogen); Site 1: EcoRI;
 Site 2: EcoRI; The library was constructed by Claire
 Murphy and Dr. James McCarter at Washington University,
 St. Louis. Oligo(dT)-SL1 PCR based library. cDNA PCR
 products of size >400 nucleotides containing SL1 on the 5'
 end and oligo(dT) on the 3' end were non-directionally
 cloned into pCRII-TOPO (Invitrogen) following the TOPO TA
 cloning protocol. Meloidogyne incognita eggs were provided
 by Andrew Kloek of Divergence Inc., St. Louis, MO."

ORIGIN

Query Match 42.6%; Score 16.6; DB 13; Length 51;
 Best Local Similarity 71.0%; Pred. No. 4.5e+04;
 Matches 22; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 6 CTGAATTTTAAACCCGAGTCAAGAGCTA 36
 |||||
 41 CTGATTTTAAAGCTTTAACTCAAGATTA 11

RESULT 7 54 bp DNA linear GSS 24-FEB-2003
 DME545095
 LOCUS
 DEFINITION Drosophila melanogaster flanking sequence of RS P element insertion
 P(RS)5-PA-1284, clone library P(RS5), genomic survey sequence.
 ACCESSION AF545095
 VERSION AF545095.1 GI:28552782
 KEYWORDS GSS; genome survey sequence.
 SOURCE Drosophila melanogaster (fruit fly)
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.

REFERENCE

1 Ryder, E.J., Ashburner, M., Baguna, J., Blows, F., Bucheton, A.,
 Coulson, D., Dickson, B., Drummond, J., Glover, D., Gunton, N.,
 Hafen, E., Hall, S., Heisenberg, M., Lepesant, J.A., Maroy, P.,
 Nechler, B., O'Kane, C., Pfeuffer, G., Rasnitsyn, A.,
 Reuter, G., Roote, J., Szidony, J., Wang, S., Webster, J. and
 Russell, S.

TITLE Mapping of RS P element insertions in Drosophila melanogaster for
 the Drosdel second generation deficiency kit

JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 54)
 AUTHORS Ryder, E.J.

COMMENT Submitted (17-FEB-2003) Ryder E.J., Department of Genetics,
 University of Cambridge, Downing Street, CB2 3EH, UNITED KINGDOM
 The insertion point of the P element is before base 1 of the
 sequence. Further information about this P element insertion line
 can be found at <http://www.flyseq.org.uk> and
<http://www.drosdel.org.uk>.

FEATURES

source

1..54
 Location/Qualifiers
 /organism="Drosophila melanogaster"
 /mol_type="genomic DNA"
 /db_xref="taxon:7227"
 /chromosome="3L"
 /clone_lib="P(RS5)"
 /clone_lib="P(RS5)"
 /note="read=5' end"
 1..54
 /note="P element insertion in the 5' to 3' orientation"

ORIGIN

Query Match 42.6%; Score 16.6; DB 29; Length 54;
 Best Local Similarity 71.0%; Pred. No. 4.5e+04;
 Matches 22; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 8 GAATTTTAAACCCGAGTCAAGAGCTAGT 38

Db 5 GAATTTTAAACCCGAGTCAAGAGCTAGT 35
 |||||

RESULT 8 53 bp DNA linear GSS 19-DEC-2003
 LOCUS CL002273/c
 DEFINITION O2S0105-04A1-A06 UniformMu Mutant Library Zea mays genomic clone
 O2S0105-04A1-A06, genomic survey sequence.

ACCESSION CL002273
 VERSION CL002273.1 GI:40219352
 KEYWORDS GSS.

SOURCE

ORGANISM Zea mays
 Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 53)
 Latshaw, S., Tan, B.-C., Settles, A.M. and McCarty, D.R.
 Sequence tagged transposon insertions from the UniformMu maize
 population

JOURNAL Unpublished (2003)
 COMMENT Contact: Donald R. McCarty

Plant Molecular and Cellular Biology Program
 University of Florida
 PO 110690 Gainesville, FL 32611-0690, USA
 Tel: 352-392-1928 x322
 Email: drmc@ufl.edu

Sequence flanking probable Mu insertion site in UniformMu line:
 O2S0105-04, primer set: A
 Class: transposon insertion site.

FEATURES

source

1..53
 Location/Qualifiers
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /strain="W22 (ACR, bz1-mg)"
 /cultivar="UniformMu"
 /db_xref="taxon:4577"
 /clone_lib="O2S0105-04A1-A06"
 /note="Vector: TOPO-PCR4; DNA flanking Mu transposon
 insertions in Mu inactive lines were extracted from the
 UniformMu maize population by the thermo asymmetric
 interlaced PCR (TAIL) protocol using primers specific for
 the Mu terminal inverted repeat and a set of 16 arbitrary
 primers. Amplicons were size enriched using Sepharose 400
 spin columns and cloned into the TOPO PCR4 vector."

ORIGIN

Query Match 42.1%; Score 16.4; DB 29; Length 53;
 Best Local Similarity 76.9%; Pred. No. 5.4e+04;
 Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 CTGAATTTTAAACCCGAGTCAAG 31
 |||||
 51 CCGAATTTCTGAACCTGATGTAAG 26

RESULT 9 60 bp DNA linear GSS 31-JAN-2003
 LOCUS BZ665081/c
 DEFINITION Arabidopsis thaliana TDNA insertion lines
 Arabidopsis thaliana genomic clone SALK_110684.14.10.x, genomic
 survey sequence.

ACCESSION BZ665081
 VERSION BZ665081.1 GI:28182384
 KEYWORDS GSS.

SOURCE

ORGANISM Arabidopsis thaliana (thale cress)
 Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 60)

REFERENCE

Query Match 41.5%; Score 16.2; DB 14; Length 57;
 Best Local Similarity 85.7%; Pred. No. 6.5e+04;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AACTGTGAATTTTAAACCC 22
 37 ACCACTGAATTTTAAACTC 57

Db 37

RESULT 12
 LOCUS B0786257 50 bp mRNA linear EST 30-AUG-2001
 DEFINITION AU106257 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
 KIA5073, mRNA sequence.
 ACCESSION AU106257
 VERSION AU106257.1 GI:13555778
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 50)
 Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
 Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
 Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
 Diverse transcriptional initiation revealed by fine, large-scale
 mapping of mRNA start sites
 EMBO Rep. 2 (5), 388-393 (2001)

TITLE JOURNAL MEDLINE 21270072
 PUBMED 11375929
 COMMENT Contact: Yutaka Suzuki
 Department of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: yusuzuki@ms.u-tokyo.ac.jp
 Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
 Sugano, S. Construction and characterization of a full
 length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
 149-156 (1997).

FEATURES
 source Location/Qualifiers
 1..50
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="KIA5073"
 /clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
 Query Match 41.0%; Score 16; DB 9; Length 50;
 Best Local Similarity 79.2%; Pred. No. 7.7e+04;
 Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 6 CTGAATTTTAAACCGAAGTCA 29
 27 CTGAACCTTTTAAACCTCCAGACA 50

Db 27

RESULT 13
 LOCUS B0786274 51 bp mRNA linear EST 26-JUL-2002
 DEFINITION Gm-c1076-4945 5', mRNA sequence.
 ACCESSION B0786274
 VERSION B0786274.1 GI:21994746
 KEYWORDS EST.
 SOURCE Glycine max (soybean)
 ORGANISM Glycine max
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 Glycine.
 1 (bases 1 to 51)
 Shoemaker, R., Keim, P., Vodkin, L., Erpelting, J., Coryell, V.,

Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, T.,
 Beck, C., Wylie, T., Underwood, K., Septice, M., Theising, B., Allen, M.,
 Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
 Schurr, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
 McCann, R., Waterston, R. and Wilson, R.
 Public Soybean EST Project
 Unpublished (1999)
 Contact: Shoemaker R/Public Soybean EST Project
 Public Soybean EST Project
 Washington University School of Medicine
 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available through: ResGen, Invitrogen Corp. 2130
 South Memorial Parkway Huntville, AL 35801 For further information
 call: (800)-533-4363 or contact: cu@resgen.com web site:
 www.resgen.com
 Seq primer: -40RP from Gibco.

FEATURES
 source Location/Qualifiers
 1..51
 /organism="Glycine max"
 /mol_type="mRNA"
 /db_xref="taxon:3847"
 /clone="SOYBEAN CLONE ID: Gm-c1076-4945"
 /tissue_type="wounded cotyledons"
 /dev_stage="11 day old seedlings"
 /lab_host="DH10B"
 /clone_lib="Gm-c1076"
 /note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
 XhoI. The cDNA library was constructed from mRNA isolated
 from 11 day old seedlings treated with that were treated
 with 2 ugs/ml of a crude glucan elicitor preparation
 isolated from the mycelial walls of Phytophthora sojae.
 The library was prepared using the Stratagene pluescript
 II SK(+) library construction kit. Complementary DNA was
 synthesized from mRNA using a primer consisting of a
 poly(dT) sequence with an xhoI restriction site. EcoRI
 adaptors were ligated to the blunt-ended cDNA fragments
 followed by XhoI digestion. The cDNA fragments were
 directionally cloned into the EcoRI-XhoI restriction site
 of the pluescript vector. The ligated cDNA fragments were
 transformed into E.coli Electorax DH10B host cells. Plant
 material was provided by Michael G. Hann (Complex
 Carbohydrate Research Center, University of Georgia) and
 the library was constructed by Anu Khanna (Talia Vodkin
 lab, University of Illinois)."

ORIGIN
 Query Match 40.5%; Score 15.8; DB 13; Length 51;
 Best Local Similarity 89.5%; Pred. No. 9.2e+04;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TAACCTGAATTTTAAAA 19
 9 TAACCTCGAATTTTAAAA 27

Db 9

RESULT 14
 LOCUS AA531325 52 bp mRNA linear EST 20-AUG-1997
 DEFINITION nj51904.s1 NCI CGAP Pr9 Homo sapiens cDNA clone IMAGE:966054
 similar to SW:NM_001038977 NADH-UBIQUINONE OXIDOREDUCTASE
 CHAIN 3 ;, mRNA sequence.
 ACCESSION AA531325
 VERSION AA531325.1 GI:2274031
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 52)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 20, 2004, 11:43:07 ; Search time 1715 Seconds

(without alignments)
985.643 Million cell updates/sec

Title: US-09-435-471B-9

Perfect score: 39
Sequence: 1 taactctgatttttaaacccgaagtcagagctagta 39

Scoring table: IDENTITY NTC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 2167151695 residues

Total number of hits satisfying chosen parameters: 1685580

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-Processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*
1: gb_da.*
2: gb_htg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vl.*
15: em_da.*
16: em_fun.*
17: em_hum.*
18: em_in.*
19: em_mu.*
20: em_om.*
21: em_ov.*
22: em_ov.*
23: em_pat.*
24: em_ph.*
25: em_pl.*
26: em_ro.*
27: em_sts.*
28: em_un.*
29: em_vl.*
30: em_htg_hum.*
31: em_htg_inv.*
32: em_htg_other.*
33: em_htg_mus.*
34: em_htg_pln.*
35: em_htg_rtd.*
36: em_htg_mam.*
37: em_htg_vrt.*
38: em_sy.*
39: em_htgo_hum.*
40: em_htgo_mus.*
41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18.6	47.7	47	6	AR288828
2	17.2	44.1	51	6	AX165073
3	17	43.6	20	6	AR076665
4	17	43.6	20	6	187134
5	17	43.6	20	6	AR182722
6	17	43.6	20	6	AR237069
7	17	43.6	20	6	AR300802
8	17	43.6	20	6	AX226320
9	17	43.6	20	6	AX774418
10	17	43.6	20	6	BD016021
11	17	43.6	20	6	BD016140
12	17	43.6	20	6	BD017292
13	16.6	42.6	32	6	AR002639
14	16.6	42.6	32	6	AR099689
15	16	41.0	47	6	AX378298
16	15.8	40.5	42	6	AX463216
17	15.8	40.5	47	6	AR288585
18	15.6	40.0	30	6	AX184137
19	15.6	40.0	43	6	AX484624
20	15.6	40.0	51	6	AX164997
21	15.4	39.5	51	6	AX158820
22	15.2	39.0	26	6	AX708066
23	15.2	39.0	35	8	AJ587623
24	15.2	39.0	38	6	AR052498
25	15.2	39.0	39	6	179583
26	15.2	39.0	41	6	AX515592
27	15.2	39.0	41	6	AX519852
28	15.2	39.0	47	6	AR284723
29	15.2	39.0	55	8	AT552810
30	15	38.5	42	6	AR154181
31	15	38.5	42	6	AR175508
32	15	38.5	42	6	AR179283
33	15	38.5	42	6	BD249391
34	15	38.5	42	6	AR352390
35	15	38.5	42	6	BD190466
36	14.8	37.9	33	6	AR034456
37	14.8	37.9	33	6	AR070401
38	14.8	37.9	33	6	AR368986
39	14.8	37.9	33	6	BD011018
40	14.8	37.9	39	6	AR014274
41	14.8	37.9	39	6	AR103029
42	14.8	37.9	39	6	E11500
43	14.8	37.9	43	6	AX483506
44	14.8	37.9	43	6	AX484539
45	14.8	37.9	46	6	AR014278

ALIGNMENTS

RESULT 1
AR288828/c
LOCUS AR288828 47 bp DNA
DEFINITION Sequence 563 from patent US 6537751.
ACCESSION AR288828
VERSION AR288828.1 GI:31676112
KEYWORDS
SOURCE
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 47)
AUTHORS Cohen D., Chumakov I. and Blumenfeld M.
TITLE Biallelic markers for use in constructing a high density
genome map of the human genome
JOURNAL Patent: US 6537751-A 563 25-MAR-2003;

FEATURES
SOURCE
Location/Qualifiers
1..47
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 47.7%; Score 18.6; DB 6; Length 47;
Best Local Similarity 68.6%; Pred. No. 4.8e+04;
Matches 24; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY
1 TAACTGATTTTAAACCCGAGTCAAGAGCT 35
46 TCACTAAATTTTTCACCTCAAGTCAATAGCT 12

Db
1 TAACTGATTTTAAACCCGAGTCAAGAGCT 35
46 TCACTAAATTTTTCACCTCAAGTCAATAGCT 12

RESULT 2
AX165073 51 bp DNA linear PAT 22-JUN-2001
LOCUS AX165073
DEFINITION Sequence 268 from Patent WO0138586.
ACCESSION AX165073
VERSION AX165073.1 GI:14545902
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1 Shimkets, R.A. and Leach, M.
Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
Patent: WO 0138586-A 268 31-MAY-2001;
JOURNAL Curagen Corporation (US)
FEATURES Location/Qualifiers
SOURCE 1..51
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
26
/note="single nucleotide polymorphism
Accession number cg4399373"

variation
Accession number cg4399373"

ORIGIN
Query Match 44.1%; Score 17.2; DB 6; Length 51;
Best Local Similarity 65.8%; Pred. No. 1.5e+05;
Matches 25; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY
2 AACTGTGATTTTAAACCCGAGTCAAGAGCTA 39
6 AATTCAGAACTTTTCAACCCGAACTGAGAGAGCA 43

Db
2 AACTGTGATTTTAAACCCGAGTCAAGAGCTA 39
6 AATTCAGAACTTTTCAACCCGAACTGAGAGAGCA 43

RESULT 3
AR076665/c 20 bp DNA linear PAT 30-AUG-2000
LOCUS AR076665
DEFINITION Sequence 30 from patent US 5959096.
ACCESSION AR076665
VERSION AR076665.1 GI:10003411
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
1 (bases 1 to 20)
REFERENCE Bennett, C. Frank, and Dean, N.
Antisense oligonucleotides against human protein kinase C
JOURNAL Patent: US 5959096-A 30 28-SEP-1999;
FEATURES Location/Qualifiers
SOURCE 1..20
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 43.6%; Score 17; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
20 CCCGAAGTCAAGAGCTA 36
20 CCCGAAGTCAAGAGCTA 4

Db
20 CCCGAAGTCAAGAGCTA 36
20 CCCGAAGTCAAGAGCTA 4

RESULT 4
187134 20 bp DNA linear PAT 10-JUN-1998
LOCUS 187134/c
DEFINITION Sequence 30 from patent US 5703054.
ACCESSION 187134
VERSION 187134.1 GI:3206852
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
1 (bases 1 to 20)
REFERENCE Bennett, C. Frank, and Dean, N.
Oligonucleotide modulation of protein kinase C
JOURNAL Patent: US 5703054-A 30 30-DEC-1997;
FEATURES Location/Qualifiers
SOURCE 1..20
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 43.6%; Score 17; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
20 CCCGAAGTCAAGAGCTA 36
20 CCCGAAGTCAAGAGCTA 4

Db
20 CCCGAAGTCAAGAGCTA 36
20 CCCGAAGTCAAGAGCTA 4

RESULT 5
AR182722/c 20 bp DNA linear PAT 20-APR-2002
LOCUS AR182722
DEFINITION Sequence 30 from patent US 6339066.
ACCESSION AR182722
VERSION AR182722.1 GI:20225929
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
1 (bases 1 to 20)
REFERENCE Bennett, C. Frank, Dean, N.M., Cook, P. Dan, and Hohe, G.
Antisense oligonucleotides which have phosphorothioate linkages of
high chiral purity and which modulate .delta.I., .beta.II., .gamma.
.delta., .EPSILON., .zeta. and .eta. isoforms of human protein
kinase C
JOURNAL Patent: US 6339066-A 30 15-JAN-2002;
FEATURES Location/Qualifiers
SOURCE 1..20
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 43.6%; Score 17; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
20 CCCGAAGTCAAGAGCTA 36
20 CCCGAAGTCAAGAGCTA 4

Db
20 CCCGAAGTCAAGAGCTA 36
20 CCCGAAGTCAAGAGCTA 4

RESULT 6
AR237069/c 20 bp DNA linear PAT 20-DEC-2002
LOCUS AR237069
DEFINITION Sequence 30 from patent US 6465439.
ACCESSION AR237069

VERSION AR237069.1 GI:27281727
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE
 1 (bases 1 to 20)
 AUTHORS Nicklin,P.L., Phillips,J.A., Love,W.G. and Hamilton,K.O.
 TITLE Pharmaceutical compositions
 JOURNAL Patent: US 6465439-A 30 15-OCT-2002;
 FEATURES
 Location/Qualifiers
 1..20
 source /organism="unknown"
 /mol_type="genomic DNA"

ORIGIN
 Query Match 43.6%; Score 17; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.2e+05;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 20 CCCGAGTCAAGAGCTA 36
 DB 20 CCCGAGTCAAGAGCTA 4

RESULT 7
 AR300802/c
 LOCUS AR300802 20 bp DNA linear PAT 12-JUN-2003
 DEFINITION Sequence 30 from patent US 6537973.
 ACCESSION AR300802
 VERSION AR300802.1 GI:31688369
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE
 1 (bases 1 to 20)
 AUTHORS Bennett,C.F., Dean,N.M., Holmlund,J.T. and Dorr,F.A.
 TITLE Oligonucleotide inhibition of protein kinase C
 JOURNAL Patent: US 6537973-A 30 25-MAR-2003;
 FEATURES
 Location/Qualifiers
 1..20
 source /organism="unknown"
 /mol_type="genomic DNA"

ORIGIN
 Query Match 43.6%; Score 17; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.2e+05;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 20 CCCGAGTCAAGAGCTA 36
 DB 20 CCCGAGTCAAGAGCTA 4

RESULT 8
 AX226320/c
 LOCUS AX226320 20 bp DNA linear PAT 10-SEP-2001
 DEFINITION Sequence 30 from Patent EP1126025.
 ACCESSION AX226320
 VERSION AX226320.1 GI:15555584
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 1
 AUTHORS Bennett,C.F. and Dean,N.
 TITLE Oligonucleotide modulation of protein kinase C
 JOURNAL Patent: EP 1126025-A 30 22-AUG-2001;
 FEATURES
 Location/Qualifiers
 1..20
 source /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"

ORIGIN /note="Artificial"

Query Match 43.6%; Score 17; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.2e+05;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 20 CCCGAGTCAAGAGCTA 36
 DB 20 CCCGAGTCAAGAGCTA 4

RESULT 9
 AX774418/c
 LOCUS AX774418 20 bp DNA linear PAT 09-JUL-2003
 DEFINITION Sequence 30 from Patent EP1310555.
 ACCESSION AX774418
 VERSION AX774418.1 GI:32486070
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 1
 AUTHORS Bennett,C.F. and Dean,N.
 TITLE Oligonucleotide modulation of protein kinase C
 JOURNAL Patent: EP 1310555-A 30 14-MAY-2003;
 FEATURES
 Location/Qualifiers
 1..20
 source /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"

ORIGIN
 Query Match 43.6%; Score 17; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.2e+05;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 20 CCCGAGTCAAGAGCTA 36
 DB 20 CCCGAGTCAAGAGCTA 4

RESULT 10
 BD016021/c
 LOCUS BD016021 20 bp DNA linear PAT 27-AUG-2002
 DEFINITION Oligonucleotide modulation of protein kinase C-epsilon.
 ACCESSION BD016021
 VERSION BD016021.1 GI:22557159
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 1 (bases 1 to 20)
 AUTHORS Bennett,F.C., Boggess,R.T. and Dean,N.M.
 TITLE Oligonucleotide modulation of protein kinase C-epsilon
 JOURNAL Patent: JP 2001224386-A 30 21-AUG-2001;
 FEATURES
 Location/Qualifiers
 1..20
 source /organism="Artificial Sequence"

COMMENT
 PN JP 2001224386-A/30
 PD 21-AUG-2001
 PF 13-DEC-2000 JP 2000379218
 PR 09-JUL-1993 US 08/089996,22-FEB-1994 US 08/199779 PI
 FRANK C BENNETT, RUSSELL T BOGGS, NICHOLAS M DEAN PC
 CLIN15/09,A61K48/00,C12Q1/48,C12Q1/68,G01N33/15,G01N33/50, PC
 G01N33/53,
 PC G01N33/566,G01N33/573//A61K31/711,A61K31/712,A61K31/7125, PC
 A61P35/00,
 PC A61P43/00,A61P43/00,C12N5/10,C12N15/00,C12N5/00 CC synthetic
 FH Key
 FT source
 Location/Qualifiers
 1..20
 source /organism="Artificial Sequence"

```

source
1. .20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 43.6%; Score 17; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 CCCGAGTCAAGAGCTA 36
DB 20 CCCGAGTCAAGAGCTA 4

RESULT 11
BD016140 20 bp DNA linear PAT 27-AUG-2002
LOCUS Oligonucleotide modulation of protein kinase C-zeta.
DEFINITION BD016140
ACCESSION BD016140.1 GI:22557278
VERSION JP 2001224387-A/30.
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE
1 (bases 1 to 20)
Bennett,F.C., Boggs,R.T. and Dean,N.M.
Oligonucleotide modulation of protein kinase C-zeta
Patent: JP 2001224387-A 30 21-AUG-2001,
ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2001224387-A/30
PC 21-AUG-2001
PF 13-DEC-2000 JP 2000379249
PR 09-JUL-1993 US 08/089996,22-FEB-1994 US 08/199779 PI
FRANK C BENNETT, RUSSELL T BOGGS, NICHOLAS M DEAN PC
C12N15/09,A61K31/7088,A61K48/00,A61P29/00,A61P35/00,A61P43/00, PC
C07H21/00,
PC C12Q1/48,C12Q1/68,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
G01N33/573//
PC C12N5/10,C12N15/00,C12N5/00
CC synthetic
FH Key Location/Qualifiers
FT source 1..20
/organism="Artificial Sequence",
Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

FEATURES
source
1. .20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 43.6%; Score 17; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 CCCGAGTCAAGAGCTA 36
DB 20 CCCGAGTCAAGAGCTA 4

RESULT 12
BD017292 20 bp DNA linear PAT 27-AUG-2002
LOCUS Oligonucleotide modulation of protein kinase C-eta.
DEFINITION BD017292
ACCESSION BD017292.1 GI:22558468
VERSION JP 2001224387-A/30.
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE
1 (bases 1 to 20)
Bennett,F.C., Boggs,R.T. and Dean,N.M.

```

```

TITLE Oligonucleotide modulation of protein kinase C-eta
JOURNAL Patent: JP 2001231579-A 30 28-AUG-2001;
COMMENT ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2001231579-A/30
PD 28-AUG-2001
PF 13-DEC-2000 JP 2000379234
PR 09-JUL-1993 US 08/089996,22-FEB-1994 US 08/199779 PI
FRANK C BENNETT, RUSSELL T BOGGS, NICHOLAS M DEAN PC
C12N15/09,A61K31/711,A61K31/712,A61K48/00,A61P29/00, PC
00,A61P35/00,
PC A61P43/00,C07H21/00,C12Q1/48,C12Q1/68,G01N33/15,G01N33/50, PC
G01N33/50,
PC G01N33/53,G01N33/566//C12N5/10,G01N33/68,C12N15/00,C12N5/00 CC
synthetic
FH Key Location/Qualifiers
FT source 1..20
/organism="Artificial Sequence",
Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

FEATURES
source
1. .20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 43.6%; Score 17; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 CCCGAGTCAAGAGCTA 36
DB 20 CCCGAGTCAAGAGCTA 4

RESULT 13
AR002639 32 bp DNA linear PAT 04-DEC-1998
LOCUS Sequence 28 from patent US 5741899.
ACCESSION AR002639
VERSION AR002639.1 GI:3964193
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE
1 (bases 1 to 32)
Capon,D.J., Tian,H., Smith,D.H., Winelow,G.A. and Siekevitz,M.
Chimeric receptors comprising janus kinase for regulating cellular
pro liferation
Patent: US 5741899-A 28 21-APR-1998;
Location/Qualifiers
1..32
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 42.6%; Score 16.6; DB 6; Length 32;
Best Local Similarity 71.0%; Pred. No. 2.8e+05;
Matches 22; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 8 GAATTTTAAACCCGAGTCAAGAGCTAGT 38
DB 32 GAGCTTCTAAACTGAGAGTCCAGAGTCACT 2

RESULT 14
AR099689 32 bp DNA linear PAT 14-FEB-2001
LOCUS AR099689
DEFINITION Sequence 28 from patent US 6077947.
ACCESSION AR099689
VERSION AR099689.1 GI:12809455
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

```

Unclassified.
1 (b)(3) (c) (1) (4) (5) (6) (7) (8) (9) (10) (11) (12) (13) (14) (15) (16) (17) (18) (19) (20) (21) (22) (23) (24) (25) (26) (27) (28) (29) (30) (31) (32) (33) (34) (35) (36) (37) (38) (39) (40) (41) (42) (43) (44) (45) (46) (47) (48) (49) (50) (51) (52) (53) (54) (55) (56) (57) (58) (59) (60) (61) (62) (63) (64) (65) (66) (67) (68) (69) (70) (71) (72) (73) (74) (75) (76) (77) (78) (79) (80) (81) (82) (83) (84) (85) (86) (87) (88) (89) (90) (91) (92) (93) (94) (95) (96) (97) (98) (99) (100) (101) (102) (103) (104) (105) (106) (107) (108) (109) (110) (111) (112) (113) (114) (115) (116) (117) (118) (119) (120) (121) (122) (123) (124) (125) (126) (127) (128) (129) (130) (131) (132) (133) (134) (135) (136) (137) (138) (139) (140) (141) (142) (143) (144) (145) (146) (147) (148) (149) (150) (151) (152) (153) (154) (155) (156) (157) (158) (159) (160) (161) (162) (163) (164) (165) (166) (167) (168) (169) (170) (171) (172) (173) (174) (175) (176) (177) (178) (179) (180) (181) (182) (183) (184) (185) (186) (187) (188) (189) (190) (191) (192) (193) (194) (195) (196) (197) (198) (199) (200) (201) (202) (203) (204) (205) (206) (207) (208) (209) (210) (211) (212) (213) (214) (215) (216) (217) (218) (219) (220) (221) (222) (223) (224) (225) (226) (227) (228) (229) (230) (231) (232) (233) (234) (235) (236) (237) (238) (239) (240) (241) (242) (243) (244) (245) (246) (247) (248) (249) (250) (251) (252) (253) (254) (255) (256) (257) (258) (259) (260) (261) (262) (263) (264) (265) (266) (267) (268) (269) (270) (271) (272) (273) (274) (275) (276) (277) (278) (279) (280) (281) (282) (283) (284) (285) (286) (287) (288) (289) (290) (291) (292) (293) (294) (295) (296) (297) (298) (299) (300) (301) (302) (303) (304) (305) (306) (307) (308) (309) (310) (311) (312) (313) (314) (315) (316) (317) (318) (319) (320) (321) (322) (323) (324) (325) (326) (327) (328) (329) (330) (331) (332) (333) (334) (335) (336) (337) (338) (339) (340) (341) (342) (343) (344) (345) (346) (347) (348) (349) (350) (351) (352) (353) (354) (355) (356) (357) (358) (359) (360) (361) (362) (363) (364) (365) (366) (367) (368) (369) (370) (371) (372) (373) (374) (375) (376) (377) (378) (379) (380) (381) (382) (383) (384) (385) (386) (387) (388) (389) (390) (391) (392) (393) (394) (395) (396) (397) (398) (399) (400) (401) (402) (403) (404) (405) (406) (407) (408) (409) (410) (411) (412) (413) (414) (415) (416) (417) (418) (419) (420) (421) (422) (423) (424) (425) (426) (427) (428) (429) (430) (431) (432) (433) (434) (435) (436) (437) (438) (439) (440) (441) (442) (443) (444) (445) (446) (447) (448) (449) (450) (451) (452) (453) (454) (455) (456) (457) (458) (459) (460) (461) (462) (463) (464) (465) (466) (467) (468) (469) (470) (471) (472) (473) (474) (475) (476) (477) (478) (479) (480) (481) (482) (483) (484) (485) (486) (487) (488) (489) (490) (491) (492) (493) (494) (495) (496) (497) (498) (499) (500) (501) (502) (503) (504) (505) (506) (507) (508) (509) (510) (511) (512) (513) (514) (515) (516) (517) (518) (519) (520) (521) (522) (523) (524) (525) (526) (527) (528) (529) (530) (531) (532) (533) (534) (535) (536) (537) (538) (539) (540) (541) (542) (543) (544) (545) (546) (547) (548) (549) (550) (551) (552) (553) (554) (555) (556) (557) (558) (559) (560) (561) (562) (563) (564) (565) (566) (567) (568) (569) (570) (571) (572) (573) (574) (575) (576) (577) (578) (579) (580) (581) (582) (583) (584) (585) (586) (587) (588) (589) (590) (591) (592) (593) (594) (595) (596) (597) (598) (599) (600) (601) (602) (603) (604) (605) (606) (607) (608) (609) (610) (611) (612) (613) (614) (615) (616) (617) (618) (619) (620) (621) (622) (623) (624) (625) (626) (627) (628) (629) (630) (631) (632) (633) (634) (635) (636) (637) (638) (639) (640) (641) (642) (643) (644) (645) (646) (647) (648) (649) (650) (651) (652) (653) (654) (655) (656) (657) (658) (659) (660) (661) (662) (663) (664) (665) (666) (667) (668) (669) (670) (671) (672) (673) (674) (675) (676) (677) (678) (679) (680) (681) (682) (683) (684) (685) (686) (687) (688) (689) (690) (691) (692) (693) (694) (695) (696) (697) (698) (699) (700) (701) (702) (703) (704) (705) (706) (707) (708) (709) (710) (711) (712) (713) (714) (715) (716) (717) (718) (719) (720) (721) (722) (723) (724) (725) (726) (727) (728) (729) (730) (731) (732) (733) (734) (735) (736) (737) (738) (739) (740) (741) (742) (743) (744) (745) (746) (747) (748) (749) (750) (751) (752) (753) (754) (755) (756) (757) (758) (759) (760) (761) (762) (763) (764) (765) (766) (767) (768) (769) (770) (771) (772) (773) (774) (775) (776) (777) (778) (779) (780) (781) (782) (783) (784) (785) (786) (787) (788) (789) (790) (791) (792) (793) (794) (795) (796) (797) (798) (799) (800) (801) (802) (803) (804) (805) (806) (807) (808) (809) (810) (811) (812) (813) (814) (815) (816) (817) (818) (819) (820) (821) (822) (823) (824) (825) (826) (827) (828) (829) (830) (831) (832) (833) (834) (835) (836) (837) (838) (839

REFERENCE 1 (bases 1 to 32)

REFERENCE	AUTHORS	TITLE
1 (bases 1 to 32)	Capon, D. J., Tian, H., Smith, D. H., Winslow, G. A. and Siekevitz, M.	DNA encoding an intracellular chimeric receptor comprising Tumor

kinase

JOURNAL Patent: US 6077947-A 28 20-JUN-2000;
FEATURES Location/Classification

source	1. .32
--------	--------

source	1. .32
--------	--------

```
/organism="unknown"
```

ORIGIN

Query Match	42.6%;	Score 16.6;	DB 6;	Length 32;
-------------	--------	-------------	-------	------------

Best Local Similarity 71.0%; Pred. No. 2.8e+05;
Matches 22; Conservative 0; Mismatches 9

Matches	22;	Conservative	0;	Mismatches	9;	Indels	0;	Gaps	0;
---------	-----	--------------	----	------------	----	--------	----	------	----

8 GAATTTTAAACCCGAAGTCAGAAGCTAGT 38

Db 32 GAGCTTCTAAACTGGAAGTCGACAGTCAGT 2

RESULT 15
AX378298/c

LOCUS	AX378298	47 bp
DEFINITION	Sequence	47 From Patent WO0205535

AX378298

VERSION AX378298.1 GT:19574148
KEYWORDS

NEIMOKDS , Homo sapiens (human)
SOURCE

ORGANISM Homo sapiens

Eukaryota; Metazoa;
Mammalia; Eutheria.

REFERENCE
1 Mammalia; Eucnecia; Filiales; Catallinini; Homilidae; Homo.

AUTHORS
Cohen, D., Blumenfeld, M., Chumakov, I., and Abderrahim, H. and Bi

TITLE Obesity associated diallelic marker maps

JOURNAL Patent: WO 0206525-A 87 24-JAN-2002:

GENSET (FR)

FEATURES	LOC
Source	1

```

2: 13)
/organism="Homo sap

```

```
/mol_type="unassigned DNA"
```

```
variation 24 /wd_xref="taxon:9606"
```

/note="99-26989-152 : polymorphic base C or T"

ORIGIN

Query Match 41.0%; Score 16; DE

Best Local Similarity 64.7%; Pred. No. 4.3e+05;

MAGEC

QY 6 CTGAATTTTAAACCCGAGTCAAGAGCTAGTA 39

[illegible]

LT WTGUTT T WWCNCT DDTADCC TTUULY Y T YNNCNCIC /

[illegible]

```

search completed: March 20, 2004, 12:53:58
Job time : 1719 secs

```

Job time : 1719 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using bw model

Run on: March 20, 2004, 06:38:30 ; Search time 38 Seconds

(without alignments)
569,555 Million cell updates/sec

Title: US-09-435-471b-9

Sequence: 1 taactctgaattttaaaccggaagtcgaagctagta 39

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 874574

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-Processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: /cgn2_6/prodata/2/ina/5A.COMB.seq:*
2: /cgn2_6/prodata/2/ina/5B.COMB.seq:*
3: /cgn2_6/prodata/2/ina/5A.COMB.seq:*
4: /cgn2_6/prodata/2/ina/5B.COMB.seq:*
5: /cgn2_6/prodata/2/ina/PCTUS.COMB.seq:*
6: /cgn2_6/prodata/2/ina/backfillseq1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18.6	47.7	47	4 US-09-422-978-563	Sequence 563, App
2	17	43.6	20	1 US-08-089-996-30	Sequence 30, App1
3	17	43.6	20	2 US-08-478-178A-30	Sequence 30, App1
4	17	43.6	20	2 US-08-488-177-30	Sequence 30, App1
5	17	43.6	20	2 US-08-481-072A-30	Sequence 30, App1
6	17	43.6	20	2 US-08-664-336-30	Sequence 30, App1
7	17	43.6	20	2 US-08-481-066A-30	Sequence 30, App1
8	17	43.6	20	3 US-08-578-615A-30	Sequence 30, App1
9	17	43.6	20	4 US-08-829-637A-30	Sequence 30, App1
10	17	43.6	20	4 US-09-254-322-30	Sequence 30, App1
11	17	43.6	20	4 US-10-025-133-30	Sequence 30, App1
12	17	43.6	20	5 PCT-US93-02213-30	Sequence 30, App1
13	17	43.6	20	5 PCT-US94-07770-30	Sequence 30, App1
14	16.6	42.6	32	1 US-08-481-003-28	Sequence 28, App1
15	16.6	42.6	32	3 US-08-485-598-28	Sequence 28, App1
16	15.8	40.5	47	4 US-09-422-978-320	Sequence 320, App
17	15.8	40.5	60	4 US-09-894-844-132	Sequence 132, App
18	15.8	40.5	60	4 US-09-894-844-132	Sequence 132, App
19	15.2	39.0	38	2 US-09-894-844-133	Sequence 133, App
20	15.2	39.0	38	2 US-08-109-923-5	Sequence 75, App1
21	15.2	39.0	37	4 US-08-433-037-7	Sequence 75, App1
22	15	38.5	42	3 US-09-671-317-775	Sequence 21, App1
23	15	38.5	42	3 US-09-290-577-21	Sequence 21, App1
24	15	38.5	42	4 US-09-290-452-21	Sequence 21, App1
25	15	38.5	42	4 US-09-290-338-21	Sequence 21, App1
26	15	38.5	42	4 US-09-290-000-21	Sequence 21, App1
27	14.8	37.9	33	2 US-09-954-594A-21	Sequence 38, App1
				2 US-08-479-275D-38	

28	14.8	37.9	33	2	US-08-488-271B-38	Sequence 38, App1
29	14.8	37.9	33	4	US-08-169-715-38	Sequence 38, App1
30	14.8	37.9	39	1	US-08-537-002A-6	Sequence 6, App1
31	14.8	37.9	39	3	US-08-863-010-6	Sequence 6, App1
32	14.8	37.9	39	3	US-09-024-429-6	Sequence 6, App1
33	14.8	37.9	46	1	US-08-537-002A-10	Sequence 10, App1
34	14.8	37.9	46	3	US-08-863-010-10	Sequence 10, App1
35	14.8	37.9	46	3	US-09-024-429-10	Sequence 10, App1
36	14.8	37.9	47	4	US-09-671-317-683	Sequence 683, App
37	14.8	37.9	50	1	US-08-171-389-517	Sequence 517, App
38	14.8	37.9	50	1	US-08-123-936-517	Sequence 517, App
39	14.8	37.9	50	2	US-08-475-228A-517	Sequence 517, App
40	14.8	37.9	50	3	US-08-482-080A-517	Sequence 517, App
41	14.8	37.9	50	4	US-09-354-947-517	Sequence 517, App
42	14.8	37.9	50	5	PCT-US93-12388-517	Sequence 517, App
43	14.6	37.4	33	1	US-08-148-058A-23	Sequence 23, App1
44	14.6	37.4	33	1	US-08-148-058A-24	Sequence 23, App1
45	14.6	37.4	33	1	US-08-478-042-23	Sequence 23, App1

ALIGNMENTS

RESULT 1
US-09-422-978-563/C
Sequence 563, Application US/09422978

Patent No. 6537751
GENERAL INFORMATION:

APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta

APPLICANT: Chumakov, Ilya
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...

FILE REFERENCE: GENSET.020CPI
CURRENT APPLICATION NUMBER: US/09/422,978

EARLIER FILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: US 09/298,850

EARLIER FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 60/109,732

EARLIER FILING DATE: 1998-11-23
EARLIER APPLICATION NUMBER: US 60/082,614

EARLIER FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796

SEQ ID NO 563
LENGTH: 47

TYPE: DNA
ORGANISM: Homo Sapiens

FEATURE:
NAME/KEY: allele

LOCATION: 24
OTHER INFORMATION: 99-15441-337 : polymorphic base A or C

US-09-422-978-563

Query Match 47.7% Score 18.6; DB 4; Length 47;
Best Local Similarity 68.6% Pred. No. 66;

Matches 24; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

Cy 1 TAACCTGAATTTTAAACCCGAGGCAAGGCT 35
Db 46 TCACATAAAATTTTTCACCTKAGTCATTAAGCT 12

RESULT 2
US-08-089-996-30/C
Sequence 30, Application US/08089996
Patent No. 5703054

GENERAL INFORMATION:
APPLICANT: Nicholas Dean, C. Frank Bennett

TITLE OF INVENTION: Oligonucleotide Modulation of Protein
NUMBER OF SEQUENCES: 62

CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz

ADDRESSEE: Mackiewicz & No. 5703054.r1s

STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/089,996
FILING DATE: 19930709
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 852,852
FILING DATE: March 16, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Rebecca Ralph Gaumont
REGISTRATION NUMBER: 35,152
REFERENCE/DOCKET NUMBER: ISIS-1154
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
ANTI-SENSE: yes
US-08-089-996-30

Query Match 43.6%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 CCCGAAGTCAAGAGCTA 36
DB 20 CCCGAAGTCAAGAGCTA 4

RESULT 3
US-08-478-178A-30/C
Sequence 30, Application US/08478178A
Patent No. 5882927
GENERAL INFORMATION:
APPLICANT: Nicholas Dean, C. Frank Bennett
TITLE OF INVENTION: Oligonucleotide Modulation of
TITLE OF INVENTION: Protein
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz
ADDRESSEE: Mackiewicz & No. 5882927
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,178A
FILING DATE: herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 852,852
FILING DATE: March 16, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Rebecca Ralph Gaumont

REGISTRATION NUMBER: 35,152
REFERENCE/DOCKET NUMBER: ISIS-1154
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
ANTI-SENSE: yes
US-08-478-178A-30

Query Match 43.6%; Score 17; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 CCCGAAGTCAAGAGCTA 36
DB 20 CCCGAAGTCAAGAGCTA 4

RESULT 4
US-08-488-177-30/C
Sequence 30, Application US/08488177
Patent No. 5885970
GENERAL INFORMATION:
APPLICANT: Nicholas Dean, C. Frank Bennett
TITLE OF INVENTION: Oligonucleotide Modulation of
TITLE OF INVENTION: Protein Kinase C
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz
ADDRESSEE: Mackiewicz & No. 5885970
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,177
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 852,852
FILING DATE: March 16, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Paul K. Legaard
REGISTRATION NUMBER: 38,534
REFERENCE/DOCKET NUMBER: ISIS-1995
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
ANTI-SENSE: yes
US-08-488-177-30

Query Match 43.6%; Score 17; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 CCCGAAGTCAAGAGCTA 36

DB 20 CCCGAAGTCAAGAGCTA 4

RESULT 5

US-08-481-072A-30/c
Sequence 30, Application US/08481072A

Patent No. 5916807

GENERAL INFORMATION:

APPLICANT: Nicholas Dean, C. Frank Bennett

TITLE OF INVENTION: Oligonucleotide Modulation of

NUMBER OF SEQUENCES: 121

CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz

ADDRESSEE: Mackiewicz & No. 5916807is

STREET: One Liberty Place - 46th Floor

CITY: Philadelphia

STATE: PA

COUNTRY: USA

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE

COMPUTER: IBM PS/2

OPERATING SYSTEM: PC-DOS

SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/481,072A

FILING DATE: herewith

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 852,852

FILING DATE: March 16, 1992

ATTORNEY/AGENT INFORMATION:

NAME: Rebecca Ralph Gaumond

REGISTRATION NUMBER: 35,152

REFERENCE/DOCKET NUMBER: ISIS-1154

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-3100

TELEFAX: (215) 568-3439

INFORMATION FOR SEQ ID NO: 30:

SEQUENCE CHARACTERISTICS:

LENGTH: 20

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

ANTI-SENSE: yes

US-08-481-072A-30

Query Match 43.6%; Score 17; DB 2; Length 20;

Best Local Similarity 100.0%; Pred. No. 2.5e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 20 CCCGAAGTCAAGAGCTA 4

QY 20 CCCGAAGTCAAGAGCTA 36

DB 20 CCCGAAGTCAAGAGCTA 4

RESULT 6

US-08-664-336-30/c

Sequence 30, Application US/08664336

Patent No. 5922686

GENERAL INFORMATION:

APPLICANT: Nicholas Dean, C. Frank Bennett

TITLE OF INVENTION: Oligonucleotide Modulation of Protein

NUMBER OF SEQUENCES: 121

CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz

ADDRESSEE: Mackiewicz & No. 5922686is

STREET: One Liberty Place - 46th Floor

CITY: Philadelphia

STATE: PA

COUNTRY: USA

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE

COMPUTER: IBM PS/2

OPERATING SYSTEM: PC-DOS

SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/481,066A

FILING DATE: herewith

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 852,852

FILING DATE: March 16, 1992

ATTORNEY/AGENT INFORMATION:

NAME: Rebecca Ralph Gaumond

REGISTRATION NUMBER: 35,152

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.5 INCH, 720 kb STORAGE

COMPUTER: IBM PS/2

OPERATING SYSTEM: PC-DOS

SOFTWARE: WORDPERFECT 6.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/664,336

FILING DATE: herewith

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 852,852

FILING DATE: March 16, 1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 089,996

FILING DATE: July 9, 1993

ATTORNEY/AGENT INFORMATION:

NAME: Paul K. Legard

REGISTRATION NUMBER: 38,534

REFERENCE/DOCKET NUMBER: ISIS-2345

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-3100

TELEFAX: (215) 568-3439

INFORMATION FOR SEQ ID NO: 30:

SEQUENCE CHARACTERISTICS:

LENGTH: 20

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

ANTI-SENSE: yes

US-08-664-336-30

Query Match 43.6%; Score 17; DB 2; Length 20;

Best Local Similarity 100.0%; Pred. No. 2.5e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 20 CCCGAAGTCAAGAGCTA 4

QY 20 CCCGAAGTCAAGAGCTA 36

DB 20 CCCGAAGTCAAGAGCTA 4

RESULT 7

US-08-481-066A-30/c

Sequence 30, Application US/08481066A

Patent No. 5959096

GENERAL INFORMATION:

APPLICANT: Nicholas Dean, C. Frank Bennett

TITLE OF INVENTION: Oligonucleotide Modulation of

NUMBER OF SEQUENCES: 121

CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz

ADDRESSEE: Mackiewicz & No. 5959096is

STREET: One Liberty Place - 46th Floor

CITY: Philadelphia

STATE: PA

COUNTRY: USA

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE

COMPUTER: IBM PS/2

OPERATING SYSTEM: PC-DOS

SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/481,066A

FILING DATE: herewith

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 852,852

FILING DATE: March 16, 1992

ATTORNEY/AGENT INFORMATION:

NAME: Rebecca Ralph Gaumond

REGISTRATION NUMBER: 35,152

REFERENCE/DOCKET NUMBER: ISIS-1154
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
ANTI-SENSE: yes
US-08-481-066A-30

Query March 43.6% Score 17; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 CCCGAAGTCAAGAGCTA 36
DB 20 CCCGAAGTCAAGAGCTA 4

RESULT 8
US-08-578-615A-30/c
Sequence 30, Application US/08578615A
Patent No. 6015892
GENERAL INFORMATION:
APPLICANT: Nicholas Dean, C. Frank Bennett and Russell, T. Boggs
TITLE OF INVENTION: Oligonucleotide Modulation of Protein Kinase C
NUMBER OF SEQUENCES: 122
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6015892ris LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/578,615A
FILING DATE: 11-JAN-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 852,852
FILING DATE: 16-MAR-1992
APPLICATION NUMBER: 08/089,996
FILING DATE: 09-JUL-1993
APPLICATION NUMBER: 08/199,779
FILING DATE: 22-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Paul K. Legaard
REGISTRATION NUMBER: 38,534
REFERENCE/DOCKET NUMBER: ISIS-1568
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
ANTI-SENSE: yes
US-08-578-615A-30

Query Match 43.6% Score 17; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 CCCGAAGTCAAGAGCTA 36
DB 20 CCCGAAGTCAAGAGCTA 4

RESULT 9
US-08-829-637A-30/c
Sequence 30, Application US/08829637A
Patent No. 6339066
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Phillip Dan Cook
APPLICANT: Nicholas Dean
APPLICANT: Glenn Hoke
TITLE OF INVENTION: OLIGONUCLEOTIDES WHICH HAVE
TITLE OF INVENTION: PHOSPHOROTHIOATE LINKAGES OF HIGH CHIRAL PURITY AND
TITLE OF INVENTION: WHICH MODULATE a1, a11, 'k, n, AND ISOFORMS OF
NUMBER OF SEQUENCES: 136
CORRESPONDENCE ADDRESS:
ADDRESSEE: John W. Caldwell (28,937) Woodcock
ADDRESSEE: Washburn Kurtz Mackiewicz & No. 6339066ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/829,637A
FILING DATE: herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/481,066
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/470,129
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/469,851
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/468,569
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/089,996
FILING DATE: 09-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/058,023
FILING DATE: 05-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/777,007
FILING DATE: 16-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/777,760
FILING DATE: 15-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/852,852
FILING DATE: 16-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/00243
FILING DATE: 11-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/566,977
FILING DATE: 13-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/436,358
FILING DATE: 11-JAN-1990
ATTORNEY/AGENT INFORMATION:

NAME:
REGISTRATION NUMBER: _____
REFERENCE/DOCKET NUMBER: ISIS-_____
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
ANTI-SENSE: yes
US-08-829-637A-30

Query Match 43.6%; Score 17; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 CCCGAAGTCAGAGCTA 36
DB 20 CCCGAAGTCAGAGCTA 4

RESULT 10
US-09-254-322-30/C
Sequence 30, Application US/09254322
PATENT No. 6465439
GENERAL INFORMATION:
APPLICANT: Nicklin, Paul
APPLICANT: Phillips, Judith
APPLICANT: Love, William
APPLICANT: Hamilton, Karen
TITLE OF INVENTION: Pharmaceutical Compositions
FILE REFERENCE: 4-21026/MA 2138/PCT
CURRENT FILING DATE: 1999-03-04
EARLIER APPLICATION NUMBER: PCT/EP97/04796
EARLIER FILING DATE: 1997-09-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 30
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-254-322-30

Query Match 43.6%; Score 17; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 CCCGAAGTCAGAGCTA 36
DB 20 CCCGAAGTCAGAGCTA 4

RESULT 11
US-10-025-139-30/C
Sequence 30, Application US/10025139
PATENT No. 6537973
GENERAL INFORMATION:
APPLICANT: Bennett, C. Frank
APPLICANT: Dean, Nicholas M.
APPLICANT: Holmlund, Jon T.
APPLICANT: Dorr, F. Andrew
TITLE OF INVENTION: Oligonucleotide Modulation Of Protein Kinase C
FILE REFERENCE: ISIS4954
CURRENT APPLICATION NUMBER: US/10/025,139
CURRENT FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: US 08/829,637

PRIOR FILING DATE: 1997-03-31
PRIOR APPLICATION NUMBER: US 08/478,178
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: US 08/089,996
PRIOR FILING DATE: 1993-07-09
PRIOR APPLICATION NUMBER: US 07/852,852
PRIOR FILING DATE: 1992-03-16
NUMBER OF SEQ ID NOS: 121
SOFTWARE: PatentIn version 3.1
SEQ ID NO 30
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-10-025-139-30

Query Match 43.6%; Score 17; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 CCCGAAGTCAGAGCTA 36
DB 20 CCCGAAGTCAGAGCTA 4

RESULT 12
PCT-US93-02213-30/C
Sequence 30, Application PC/TUS9302213
GENERAL INFORMATION:
APPLICANT: Nicholas Dean, C. Frank Bennett
TITLE OF INVENTION: Oligonucleotide Modulation of Protein
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSER: Woodcock Washburn Kurtz
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/02213
FILING DATE: 19930225
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 852,852
FILING DATE: March 16, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: ISIS-0872
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
ANTI-SENSE: yes
PCT-US93-02213-30

Query Match 43.6%; Score 17; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 CCCGAAGTCAAGAGCTA 36
|||||
Db 20 CCCGAAGTCAAGAGCTA 4

RESULT 13

PCT-US94-07770-30/C
Sequence 30, Application PC/TUS9407770
GENERAL INFORMATION:
APPLICANT: Nicholas Dean, C. Frank Bennett and
APPLICANT: Russell T. Boggs
TITLE OF INVENTION: Oligonucleotide Modulation of
TITLE OF INVENTION: Protein Kinase C
NUMBER OF SEQUENCES: 119
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz
ADDRESSEE: Mackiewicz & Norris
STREET: One Liberty Place - 46th Floor
City: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb
MEDIUM TYPE: STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07770
FILING DATE: herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 952,852
FILING DATE: March 16, 1992
APPLICATION NUMBER: 08/089,996
FILING DATE: July 9, 1993
APPLICATION NUMBER: 08/199,779
FILING DATE: February 22, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Rebecca Ralph Gaumont
REGISTRATION/DOCKET NUMBER: 35,152
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
ANTI-SENSE: yes
PCT-US94-07770-30

Query Match 43.6%; Score 17; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 CCCGAAGTCAAGAGCTA 36
|||||
Db 20 CCCGAAGTCAAGAGCTA 4

RESULT 14

US-08-481-003-28/C
Sequence 28, Application US/08481003
Patent No. 5741899
GENERAL INFORMATION:
APPLICANT: CAPON, DANIEL J
APPLICANT: TIAN, HUAN
APPLICANT: SMITH, DOUGLAS H

APPLICANT: WINSLOW, GENINE A
APPLICANT: SIKSEVITZ, MIRIAM
TITLE OF INVENTION: CHIMERIC RECEPTORS FOR REGULATING
TITLE OF INVENTION: CELLULAR PROLIFERATION AND EFFECTOR FUNCTION
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: CELL GENESYS, INC.
STREET: 322 LAKESIDE DRIVE
CITY: FOSTER CITY
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94404

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,003
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/382,846
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: KRUPEN, KAREN I
REGISTRATION NUMBER: 34,647
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 358-9600 x131
TELEFAX: (415) 349-7392
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

US-08-481-003-28

Query Match 42.6%; Score 16.6; DB 1; Length 32;
Best Local Similarity 71.0%; Pred. No. 4.1e+02;
Matches 22; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 8 GAATTTTAAACCCGAAGTCAAGAGCTAGT 38
|||||
Db 32 GAGCTTCTAAAGTGAAGTCAAGAGCTAGT 2

RESULT 15

US-08-485-598-28/C
Sequence 28, Application US/08485598
Patent No. 6077947
GENERAL INFORMATION:
APPLICANT: CAPON, DANIEL J
APPLICANT: TIAN, HUAN
APPLICANT: SMITH, DOUGLAS H
APPLICANT: WINSLOW, GENINE A
APPLICANT: SIKSEVITZ, MIRIAM
TITLE OF INVENTION: CHIMERIC RECEPTORS FOR REGULATING
TITLE OF INVENTION: CELLULAR PROLIFERATION AND EFFECTOR FUNCTION
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: CELL GENESYS, INC.
STREET: 322 LAKESIDE DRIVE
CITY: FOSTER CITY
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94404

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

```

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,598
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/382,846
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: KRUPEN, KAREN I
REGISTRATION NUMBER: 34,647
REFERENCE/DOCKET NUMBER: CELL 17
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 358-9600 x131
TELEFAX: (415) 349-7392
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-485-598-28

```

```

Query Match          42.6%; Score 16.6; DB 3; Length 32;
Best Local Similarity 71.0%; Pred. No. 4.1e+02;
Matches 22; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

```

```

QY      8 GAATTTTAAACCCGAGTCAAGAGCTAGT 38
Db      32 GAGCTTCTAAACTGGAAGTCGACAGTCAGT 2

```

Search completed: March 20, 2004, 08:43:33
Job time : 40 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 20, 2004, 08:43:35 ; Search time 243 Seconds

(without alignments)
681.810 Million cell updates/sec

Title: US-09-435-471B-9

Sequence: 1 taacctgaatttttaaacccgaagtcagaagctagta 39

Scoring table: IDENTITY_NTC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 segs, 2124099041 residues

Total number of hits satisfying chosen parameters: 3309108

Minimum DB seq length: 0

Maximum DB seq length: 60

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19.4	49.7	50	6	ABZ05319 Human leu
2	17.4	44.6	47	3	Az66216 Human map
3	17.2	44.1	51	5	Ab100277 Human spl
4	17	43.6	20	2	AAG49686 PKC-Beta
5	17	43.6	20	2	AAG97903 PNA oligo
6	17	43.6	20	2	AAG84190 PKC-Beta
7	17	43.6	20	2	AAX35530 Oligo ON3
8	17	43.6	20	2	AAX22591 Human pro
9	17	43.6	20	2	AAX78553 Human pro
10	17	43.6	20	2	AAX83662 Human pro
11	17	43.6	20	2	AAX19156 Human PKC
12	17	43.6	20	2	AAX27295 Human pro
13	17	43.6	20	6	Ab190883 Human pro
14	17	43.6	20	4	ACH11162 Human pro
15	17	43.6	26	4	Aaf70175 Human TNF
16	16.8	43.1	50	6	Abz05655 Human leu
17	16.6	42.6	32	2	AAT13501 PCR prime
18	16.6	42.6	51	4	AAT27388 Human SNP
19	16	41.0	25	8	AC101214 Human mic
20	16	41.0	47	6	ABK40839 Human obo
21	15.8	40.5	42	6	ABQ82194 Human CD8
22	15.8	40.5	45	4	AAC82264 Human ret
23	15.8	40.5	50	6	ABZ02741 Human leu

24	15.8	40.5	50	6	ABZ01361 Human leu
25	15.8	40.5	50	6	ABZ04957 Human leu
26	15.8	40.5	60	6	ABN40377 Human spl
27	15.6	40.0	25	8	AC119196 Human mic
28	15.6	40.0	30	4	AAH91564 Human inf
29	15.6	40.0	41	6	ABZ49267 Human aid
30	15.6	40.0	41	6	ABZ45006 Human aid
31	15.6	40.0	43	6	ABZ27977 Candida e
32	15.6	40.0	50	7	ACB83177 PCR prime
33	15.6	40.0	51	5	AB100201 Human spl
34	15.4	39.5	31	2	AAV67919 Nucleotid
35	15.4	39.5	51	4	AAT75207 Human sil
36	15.4	39.5	60	6	ABN39178 Human spl
37	15.2	39.0	26	7	ACC90636 Human cyp
38	15.2	39.0	38	2	AAT84539 BIRK 10 p
39	15.2	39.0	41	6	AB142413 IL factor
40	15.2	39.0	51	4	AA132249 Human SNP
41	15.2	39.0	56	2	AAX11567 Human bta
42	15	38.5	42	3	AAC64821 Novel str
43	15	38.5	42	3	AAC63142 Novel str
44	15	38.5	42	3	AAC65232 Allele-sp
45	15	38.5	42	3	AAC65165 Novel str

ALIGNMENTS

RESULT 1
ABZ05319
ID ABZ05319 standard; DNA; 50 BP.
XX
AC ABZ05319;
XX
DT 09-JAN-2003 (first entry)
XX
DE Human leukocyte gene expression profiling probe SEQ ID NO 5310.
XX
KW T7; leukocyte; gene expression profiling; allograft rejection;
KW atherosclerosis; congestive heart failure; systemic lupus erythematosus;
KW rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
KW ss.
XX
OS Homo sapiens.
XX
PN WO200257414-A2.
XX
PD 25-JUL-2002.
XX
PF 22-OCT-2001; 2001WO-US047856.
XX
PR 20-OCT-2000; 2000US-0241994P.
XX
PR 08-JUN-2001; 2001US-0296764P.
XX
PA (BIOC-) BIOCARDIA INC.
XX
PI Mohlgemuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J;
PI Ly N, Woodward R, Quetermours T, Johnson F;
PI MPI; 2002-63625/68.
XX
DR New system for leukocyte expression profiling, diagnosing a disease, or
PT monitoring (the rate of) progression of a disease, e.g. atherosclerosis
PT or congestive heart failure, comprises diagnostic oligonucleotides.
XX
PS Claim 1; Page 499; Opp; English.
XX
CC The invention relates to a system for detecting gene expression, which
CC comprises one or two isolated DNA molecules that detect expression of a
CC gene, where the gene corresponds to any of 8143 oligonucleotides
CC (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful
CC for leukocyte expression profiling. It is particularly useful for
CC diagnosing a disease, monitoring (rate of) progression of a disease,
CC predicting therapeutic outcome, determining prognosis for a patient,

CC predicting disease complications in an individual or monitoring response
CC to treatment in an individual. The diseases include cardiac allograft
CC rejection, kidney allograft rejection, liver allograft rejection,
CC atherosclerosis, congestive heart failure, systemic lupus erythematosus,
CC rheumatoid arthritis, osteoarthritis or cytomegalovirus infection
XX
SQ Sequence 50 BP, 15 A, 11 C, 7 G, 17 T, 0 U, 0 Other;
Query Match 49.7%; Score 19.4; DB 6; Length 50;
Best Local Similarity 79.3%; Pred. No. 3.6e+02;
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 2 AACTCTGAATTTTAAACCCGAGTCAA 30
4 AAGTTGAAATTGTCAATCCCAAGTCAA 32
Db
RESULT 2
AAZ66216/c
ID AAZ66216 standard; DNA; 47 BP.
XX
AC AAZ66216;
XX
DT 10-SEP-2001 (first entry)
DE Human map-related diallelic marker SEQ ID NO:563.
XX
XX Human genome; diallelic marker; high density disequilibrium map;
KM genomic map; haplotype; phenotype; polymorphic base; genotyping;
KM haplotyping; hybridisation; identification; characterisation; diagnosis;
KM single nucleotide polymorphism; SNP; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT variation replace(24,C)
FT /*tag= a
FT /standard_name= "single nucleotide polymorphism"
XX
XX WO9954500-A2.
XX
PD 28-OCT-1999.
XX
PF 21-APR-1999; 99WO-IB000822.
XX
PR 21-APR-1998; 98US-0082614P.
PR 23-NOV-1998; 98US-0109732P.
XX
XX (GENSET).
XX
PI Cohen D, Blumenfeld M, Chumakov I,
XX
XX WPI; 2000-0133267/01.
XX
PT Novel diallelic markers used to construct a high density disequilibrium
PT map of the human genome.
XX
PS Claim 1; Page 350; 2745pp; English.
XX
XX AAZ65654 to AAZ69578 represent human diallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC primers for the diallelic markers. The diallelic markers of the invention
CC have a variety of uses: they can be used for high density mapping of the
CC human genome, and in complex association studies and haplotyping studies
CC which are useful in determining the genetic basis for disease states.
CC Compositions and methods of the invention can also be useful for the
CC identification of the targets for the development of pharmaceutical
CC agents and diagnostic methods, as well as the characterisation of the
CC differential efficacious responses to and side effects from
CC pharmaceutical agents acting on a disease as well as other treatment.
CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
CC 3367, are not actually given a sequence in the Sequence Listing from the

CC present invention
XX
SQ Sequence 47 BP, 19 A, 2 C, 12 G, 14 T, 0 U, 0 Other;
Query Match 44.6%; Score 17.4; DB 3; Length 47;
Best Local Similarity 68.6%; Pred. No. 2.3e+03;
Matches 24; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY 1 TAACTCTGAATTTTAAACCCGAGTCAAAGCT 35
46 TCACATAAAATTTTTCACCTTAAGTCATAAGCT 12
Db
RESULT 3
ABL00277
ID ABL00277 standard; DNA; 51 BP.
XX
AC ABL00277;
XX
DT 05-MAR-2002 (first entry)
DE Human silent noncoding SNP oligonucleotide SEQ ID NO:268.
XX
XX Human; single nucleotide polymorphism; SNP; polymorphism; cytostatic;
KM immunosuppressive; antiinflammatory; neuroprotective; antimicrobial;
KM autoimmune disease; inflammation; cancer; nervous system disease;
KM infection; polymorphic protein; ds.
XX
OS Homo sapiens.
XX
PN WO200138586-A2.
XX
PD 31-MAY-2001.
XX
PF 22-NOV-2000; 2000MO-US032311.
XX
PR 24-NOV-1999; 99US-0167383P.
XX
XX (CURA-) CURAGEN CORP.
XX
PI Shinkets RA, Leach M;
XX
XX WPI; 2001-355949/37.
XX
XX Isolated human nucleic acids comprising one or more single nucleotide
PT polymorphisms, useful for treating a subject suffering from a pathology,
PT e.g. autoimmune diseases, ascribed to the presence of a sequence
PT polymorphism.
XX
PS Claim 1; Page 328; 674pp; English.
XX
XX ABL00010 to ABL01104 represent human nucleic acid oligonucleotides
CC comprising one or more single nucleotide polymorphisms (SNPs). ABB56531
CC to ABB56903 represent human peptides encoded by some of the SNP
CC oligonucleotides. The sequences from the present invention can have
CC immunosuppressive, cytostatic, antiinflammatory, neuroprotective and
CC antimicrobial activities. Nucleic acids, polypeptides, oligonucleotides
CC and antibodies from the present invention can be used for treating a
CC subject suffering from, at risk for, or suspected of, suffering from a
CC pathology ascribed to the presence of a sequence polymorphism. The
CC pathology may be autoimmune diseases, inflammation, cancer, diseases of
CC the nervous system, and infection by pathogenic microorganisms. The SNPs
CC are also useful for determining which forms of a characterised
CC polymorphism are present in individuals. The antibodies may be used in
CC the detection, quantitation and/or cellular or tissue localisation of a
CC polymorphic protein (e.g., for use in measuring levels of the polymorphic
CC protein within appropriate physiological samples)
XX
SQ Sequence 51 BP, 16 A, 15 C, 10 G, 10 T, 0 U, 0 Other;
Query Match 44.1%; Score 17.2; DB 5; Length 51;
Best Local Similarity 65.8%; Pred. No. 2.8e+03;
Matches 25; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Db 20 CCGAAGTCAAGAGCTA 4

RESULT 6

AA084190/c
ID AA084190 standard; DNA; 20 BP.

XX AA084190;

XX 25-MAR-2003 (revised)

XX 21-SEP-1995 (first entry)

XX PKC-beta type II antisense oligo, binds to cDNA bases 2141-2160.

XX Antisense; protein kinase C; alpha; PKC; beta; gamma; eta; epsilon; zeta;

XX modulation; expression; isozyme; hybridise; 5' UTR; human;

XX 3' untranslated region; translation initiation site; detection;

XX phosphorothioate linkage; 2'-O-methyl modification;

XX 2'-O-propyl modification; ss.

XX Synthetic.

XX MO9502069-A1.

XX 19-JAN-1995.

XX 08-JUL-1994; 94WO-US007770.

XX 09-JUL-1993; 93US-00089996.

XX 22-FEB-1994; 94US-00199779.

XX (ISIS-) ISIS PHARM INC.

XX Bennett CF, Boggs RT, Dean NM;

XX WPI; 1995-066911/09.

XX Oligo:nucleotide(s) hybridisable with Protein Kinase C mRNA or gene -

XX also novel PKC-alpha 3'-UTR sequence, useful for diagnosis and treatment

XX of hyperproliferative disorders.

XX Claim 13; Page 27; 125pp; English.

XX The sequences given in AA084190-94 are oligos which are antisense to the

XX protein kinase C-beta (PKC-beta) type II cDNA. These oligos are antisense

XX to regions in the 3' untranslated region of the cDNA. The type I and type

XX II PKC-beta cDNA's are identical at the 5' end but diverge at the 3' end.

XX These antisense molecules may be used in modulating the expression of

XX the 5'- or 3'-untranslated regions of the PKC gene, or the translation

XX initiation site, or the coding region. These oligos may be used in the

XX detection of the human PKC genes and for treatment of animals which have

XX conditions associated with PKC, esp. hyperproliferative diseases such as

XX psoriasis, colorectal cancer, lung cancer, breast or skin cancer. These

XX oligos may contain at least one phosphorothioate linkage and/or at least

XX one of the nucleotides comprises a modification on the 2' position of the

XX sugar, esp. a 2'-O-methyl or a 2'-O-propyl modification. (Updated on 25-

XX MAR-2003 to correct PN field.)

XX Sequence 20 BP; 3 A; 5 C; 5 G; 7 T; 0 U; 0 Other;

XX Query Match 43.6%; Score 17; DB 2; Length 20;

XX Best Local Similarity 100.0%; Pred. No. 2.9e+03;

XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 20 CCGAAGTCAAGAGCTA 36

XX Db 20 CCGAAGTCAAGAGCTA 4

XX RESULT 7

XX AAV35530/c

ID AAV35530 standard; DNA; 20 BP.

XX AAV35530;

XX 01-SEP-1998 (first entry)

XX Oligo ON30 targeted to human protein kinase C (PKC)-beta type II.

XX Protein kinase C; PKC; target; hybridisation; human; liposome;

XX sterically stabilised; neoplastic disorder; inflammatory disorder;

XX hyperproliferative disorder; cancer; psoriasis; PKC-beta; ss.

XX Synthetic.

XX Homo sapiens.

XX MO9809633-A2.

XX 12-MAR-1998.

XX 03-SEP-1997; 97WO-EP004796.

XX 04-SEP-1996; 96GB-00018376.

XX (NOVS) NOVARTIS AG.

XX Nicklin PL, Phillips JA, Love WG, Hamilton KO;

XX WPI; 1998-260955/23.

XX Oligo:nucleotide compositions for protein kinase C disorders - comprising

XX sequence hybridisable to protein kinase C gene entrapped in sterically

XX stabilised liposomes.

XX Claim 21; Page 8; 25pp; English.

XX This represents an oligonucleotide sequence that is specifically

XX hybridisable with DNA or RNA derived from a protein kinase C (PKC) gene,

XX entrapped in sterically stabilised liposomes. Compositions comprising

XX such oligonucleotides can be used in the treatment of PKC disorders and

XX for modulating the expression of PKC in cells. They can be used in the

XX diagnosis and treatment of disorders associated with PKC, particularly

XX neoplastic, inflammatory and hyperproliferative disorders such as cancer

XX or psoriasis. The compositions retain high activity after prolonged

XX circulation in the bloodstream and exhibit reduced accumulation of

XX oligonucleotides in non-target organs such as the liver and kidney

XX Sequence 20 BP; 3 A; 5 C; 5 G; 7 T; 0 U; 0 Other;

XX Query Match 43.6%; Score 17; DB 2; Length 20;

XX Best Local Similarity 100.0%; Pred. No. 2.9e+03;

XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 20 CCGAAGTCAAGAGCTA 36

XX Db 20 CCGAAGTCAAGAGCTA 4

XX RESULT 8

XX AAX22591/c

XX AAX22591 standard; DNA; 20 BP.

XX AAX22591;

XX 27-MAY-1999 (first entry)

XX Human protein kinase C antisense oligonucleotide #30.

XX Protein kinase C; PKC; human; antisense; primer; inhibitor; treatment;

XX hyperproliferative condition; cancer; colorectal; breast; bladder; lung;

XX brain; glioblastoma multiforme; skin; psoriasis; ss.

XX Synthetic.

XX Homo sapiens.

XX US5885970-A.
XX 23-MAR-1999.
XX 07-JUN-1995; 95US-00488177.
XX 16-MAR-1992; 92US-00852852.
XX 09-JUL-1993; 93US-00089996.
XX (ISIS-) ISIS PHARM INC.
XX Dean N, Bennett CF;
XX WPI, 1999-228583/19.
XX New human protein kinase C antisense oligonucleotides - useful for
XX treating PKC-related hyperproliferative conditions e.g. cancer and
XX psoriasis.
XX Example 4; Col 15; 55pp; English.
XX This invention describes antisense oligonucleotides that specifically
XX bind to human protein kinase C (PKC) mRNA. These oligonucleotides can be
XX used to inhibit PKC mRNA and therefore be used to treat PKC-related
XX hyperproliferative conditions, e.g. cancer, especially colorectal cancer,
XX breast cancer, bladder cancer, lung cancer, or brain cancer (preferably
XX glioblastoma multiforme). The products of the invention may also be used
XX to treat skin cancer and psoriasis
XX Sequence 20 BP; 3 A; 5 C; 5 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 43.6%; Score 17; DB 2; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 2.9e+03;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 20 CCCGAAGTCAGAGCTA 36
XX 20 CCCGAAGTCAGAGCTA 4
XX
XX RESULT 9
XX AAX78553/c
XX ID AAX78553 standard; DNA; 20 BP.
XX AAX78553;
XX 03-SEP-1999 (first entry)
XX Human PKC-beta type II oligonucleotide primer #1.
XX PKC; human; PKC-alpha; primer; protein kinase C; expression modulator;
XX PKC-beta type I; PKC-beta type II; PKC-gamma; PKC-eta; PKC-delta;
XX PKC-epsilon; PKC-zeta; anti-inflammatory; cytostatic;
XX antisense targeting; isozyme; growth control; hyperproliferative disease;
XX colon cancer; glioblastoma; bladder cancer; inflammatory condition;
XX psoriasis; ss.
XX Synthetic.
XX Homo sapiens.
XX US5922686-A.
XX 13-JUL-1999.
XX 14-JUN-1996; 96US-00664336.
XX 16-MAR-1992; 92US-00852852.
XX 09-JUL-1993; 93US-00089996.
XX (ISIS-) ISIS PHARM INC.
XX Dean N, Bennett CF;
XX

XX DR WPI, 1999-404471/34.
XX Oligonucleotides targeted against nucleic acids encoding protein kinase
XX C.
XX Example 4; Col 41-42; 56pp; English.
XX This invention describes novel oligonucleotides (AAX78524-X78644) having
XX up to 50 nucleotides hybridisable with, and able to modulate the
XX expression of, a nucleic acid encoding protein kinase C and its isozymes
XX Alpha, beta type I, beta type II, gamma, eta, delta, epsilon and zeta.
XX The oligonucleotides of the invention have anti-inflammatory and
XX cytostatic activity and are used for antisense targeting to modulate the
XX expression of PKC or of a particular PKC isozyme or set of isozymes in
XX cells or tissues. The products of the invention also hybridise with
XX nucleic acids involved in the modulation of PKC expression, which is
XX known to be involved in growth control in hyperproliferative diseases e.g.
XX colon cancer, glioblastoma and bladder cancer as well as in inflammatory
XX conditions e.g. psoriasis. Due to their specificity the oligonucleotides
XX are able to overcome the problems of toxicity associated with previous
XX agents designed to modulate PKC expression
XX Sequence 20 BP; 3 A; 5 C; 5 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 43.6%; Score 17; DB 2; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 2.9e+03;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 20 CCCGAAGTCAGAGCTA 36
XX 20 CCCGAAGTCAGAGCTA 4
XX
XX RESULT 10
XX AAX83662/c
XX ID AAX83662 standard; DNA; 20 BP.
XX AAX83662;
XX 27-AUG-1999 (first entry)
XX Human protein kinase C antisense oligonucleotide SEQ ID NO:30.
XX Human; protein kinase C; PKC; antisense oligonucleotide; diagnosis; ss;
XX hybridisation; cancer; psoriasis; hyperproliferative disease; tumour.
XX Synthetic.
XX Homo sapiens.
XX US5916807-A.
XX 29-JUN-1999.
XX 07-JUN-1995; 95US-00481072.
XX 16-MAR-1992; 92US-00852852.
XX 09-JUL-1993; 93US-00089996.
XX (ISIS-) ISIS PHARM INC.
XX Dean N, Bennett CF;
XX WPI, 1999-403817/34.
XX New antisense oligonucleotides specific for human protein kinase C useful
XX for diagnosis and treatment of cancer and psoriasis.
XX Claim 1; Col 15; 54pp; English.
XX The present invention describes a method of inhibiting the expression of
XX human protein kinase C (PKC) in cells. The method comprises contacting
XX the cells with an antisense oligonucleotide which has up to 50 nucleotide

CC unite. AAX83633 to AAX83720 represent specifically claimed antisense
CC oligonucleotides for use in the method of the invention. The antisense
CC oligonucleotides modulate hybridize to messenger RNA from the PKC gene
CC which results in modulation of expression of the PKC gene. This means
CC they can be used for diagnosis, therapeutic or prophylactic treatment of
CC PKC associated diseases such as cancer and psoriasis, and as research
CC agents. Abnormal proliferative states in tissue from patients suspected
CC of having a hyperproliferative disease e.g. cancer, psoriasis can be
CC diagnosed. Tumours associated with PKC can be distinguished from tumours
CC which are not PKC associated to allow an efficacious treatment regime to
CC be used. The antisense oligonucleotides have specific activity so are
CC able to modulate PKC activity without producing side effects and with
CC greater effectiveness than observed from administration of current
CC agents. AAX83721 to AAX83753 represent other oligonucleotides used in
CC examples from the present invention

XX
SQ Sequence 20 BP; 3 A; 5 C; 5 G; 7 T; 0 U; 0 Other;
Query Match 43.6%; Score 17; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 CCCGAAGTCAGAGCTA 36
Db 20 CCCGAAGTCAGAGCTA 4

RESULT 11
AAX19156/c
ID AAX19156 standard; DNA; 20 BP.
XX
AC AAX19156;
XX
DT 20-MAR-2003 (revised)
DT 14-MAY-1999 (first entry)
XX
DE Human PKC-beta type II antisense oligonucleotide SEQ ID NO:30.
XX
KW Human; PKC; protein kinase C; diagnosis; antisense oligonucleotide;
KW phosphothioate linkage; hyperproliferative disease; cancer; psoriasis;
KW tumour; inhibition; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN US5882927-A.
XX
PD 16-MAR-1999.
XX
PE 07-JUN-1995; 95US-00478178.
XX
PR 16-MAR-1992; 92US-00852852.
PR 09-JUL-1993; 93US-00089996.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Dean N, Bennett CF;
XX
PT WPI; 1999-214073/18.
XX
DR
XX
PT New synthetic oligonucleotides inhibiting expression of protein kinase C
PT (PKC)-alpha - useful for treating and diagnosing conditions associated
PT with abnormal PKC expression.
XX
PS Example 4; Col 16; 56pp; English.
XX
CC The present invention specifically describes antisense oligonucleotides
CC of up to 50 nucleotides in length which specifically bind human protein
CC kinase C-alpha (PKC-alpha) mRNA. AAX19127 to AAX19247 represent antisense
CC oligonucleotides from the present invention which bind human PKC-alpha,
CC beta, -gamma, -delta, -epsilon, -zeta and -eta. The antisense
CC oligonucleotides modulate the expression of the PKC gene (i.e. inhibit
CC the PKC gene). The antisense oligonucleotides can be used to diagnose

CC abnormal proliferative states in tissue or other samples from patients
CC suspected of having a hyperproliferative disease e.g. cancer or psoriasis.
CC The antisense oligonucleotides can be used to distinguish PKC-associated
CC tumours and to detect and diagnose PKC expression (through the use of 32P
CC labeled antisense oligonucleotides). Radiolabeled antisense
CC oligonucleotides can also be used to perform autoradiography of tissues
CC to determine the localization, distribution and quantitation of PKC
CC expression for research, diagnostic and therapeutic purposes. The use of
CC the antisense oligonucleotides eliminate the side effects associated with
CC prior art methods because it modulates the amount of PKC protein made
CC from the gene rather than inhibiting the enzyme itself. (Updated on 20-
CC MAR-2003 to correct PF field.)

XX
SQ Sequence 20 BP; 3 A; 5 C; 5 G; 7 T; 0 U; 0 Other;
Query Match 43.6%; Score 17; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 CCCGAAGTCAGAGCTA 36
Db 20 CCCGAAGTCAGAGCTA 4

RESULT 12
AAZ27295/c
ID AAZ27295 standard; DNA; 20 BP.
XX
AC AAZ27295;
XX
DT 01-DEC-1999 (first entry)
XX
DE Human protein kinase C beta antisense oligonucleotide #10.
XX
KW Human; protein kinase C; PKC; diagnosis; antisense oligonucleotide;
KW phosphothioate; hybridisation; isozyme; target; inflammation;
KW hyperproliferative disorder; psoriasis; tumour; cancer; glioblastoma; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN US5959096-A.
XX
PD 28-SEP-1999.
XX
PE 07-JUN-1995; 95US-00481066.
XX
PR 16-MAR-1992; 92US-00852852.
PR 09-JUL-1993; 93US-00089996.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Bennett CF, Dean N;
XX
PT WPI; 1999-561076/47.
XX
DR
XX
PT Antisense oligonucleotides useful for treatment of hyperproliferative and
PT inflammatory conditions including psoriasis, tumors and cancer.
XX
PS Claim 1; Col 15; 56pp; English.
XX
CC The present invention describes antisense oligonucleotides up to 50
CC nucleotides in length which specifically bind mRNA encoding human protein
CC kinase C (PKC). AAZ27266 to AAZ27386 represent human PKC antisense
CC oligonucleotides used in the exemplification of the present invention.
CC The antisense oligonucleotides are useful for the treatment of diseases
CC associated with PKC expression, such as hyperproliferative and
CC inflammatory conditions including psoriasis, tumours and cancer
CC (glioblastoma, bladder, breast, colon and lung cancer)

XX
SQ Sequence 20 BP; 3 A; 5 C; 5 G; 7 T; 0 U; 0 Other;
Query Match 43.6%; Score 17; DB 2; Length 20;

Query Match 43.6%; Score 17; DB 6; Length 20;

RESULT 15
AAEF70175

ID	AAF70175 standard; DNA; 26 BP
XX	

AC	AA70175;
XX	
DT	18-APR-2001 (first entry)
XX	
DE	Human TNFRSF11B gene promoter fragment 3 PCR primer.
XX	
KW	Human; TNFRSF11B; osteoclastogenesis inhibitory factor;
KW	single nucleotide polymorphism; SNP; osteoclast recruitment;
KW	osteoclast function; osteoporosis; metastatic bone disease;
KW	Paget's disease; rheumatoid arthritis; periodontal bone disease;
KW	PCR primer; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO200104137-A1.
XX	
PD	18-JAN-2001.
XX	
PF	10-JUL-2000; 2000WO-US018803.
XX	
PR	09-JUL-1999; 99US-0143020P.
XX	
PA	(GENA-) GENAISSANCE PHARM INC.
XX	
PI	Chew A, Denton RR, Duda A, Nandabalan K, Stephens JC;
XX	
DR	WPI; 2001-147175/15.
XX	
PT	Human Osteoclastogenesis Inhibitory Factor nucleotides, comprising single
XX	nucleotide polymorphisms, useful for studying e.g. osteoporosis, Paget's
PT	disease and rheumatoid arthritis.
XX	
PS	Example 1B; Page 38; 114pp; English.
XX	
CC	The present sequence is a primer used to isolate polymorphic regions of
CC	the human osteoclastogenesis inhibitory factor (TNFRSF11B).
CC	Polynucleotides comprising one or more of twenty four novel single
CC	nucleotide polymorphisms in the TNFRSF11B gene have been identified.
CC	TNFRSF11B regulate osteoclast recruitment and function. An understanding
CC	of variations in the gene should thus be useful in developing new
CC	therapies for metabolic disorders caused by abnormal osteoclast
CC	recruitment and function such as osteoporosis, metastatic bone disease,
CC	Paget's disease, rheumatoid arthritis and periodontal bone disease
XX	
XX	
SO	Sequence 26 BP; 8 A; 4 C; 8 G; 6 T; 0 U; 0 Other;
	Query Match 43.6%; Score 17; DB 4; Length 26;
	Best Local Similarity 80.0%; Pred. No. 3e+03;
	Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0
OY	7 TGAATTTTAAACCCGAAAGTCAG 31
DB	2 TGAAGTTTCAGAACCCGAAAGTGAAG 26

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 20, 2004, 08:36:30 ; Search time 195 Seconds

(without alignments)
739.831 Million cell updates/sec

Title: US-09-435-471B-9

Sequence: 1 taactctgaattttaaaccagagtaagagctagta 39

Scoring table: IDENTITY_NUC

Gapop 10.0 ; Gapext 1.0

Searched: 2438257 seqs, 1849576744 residues

Total number of hits satisfying chosen parameters: 1466766

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	19.4	49.7	50	US-10-131-827-5310	Sequence 5310, App
2	18.6	47.7	47	US-10-349-143-563	Sequence 563, App
3	17	43.6	20	US-10-348-485-30	Sequence 30, Appl
4	16.8	43.1	50	US-10-131-827-5650	Sequence 5650, App
5	16	41.0	25	US-10-098-263B-1205	Sequence 1205, App
6	16	41.0	47	US-10-333-429-87	Sequence 87, Appl
7	15.8	40.5	42	US-10-025-367-17	Sequence 17, Appl
8	15.8	40.5	47	US-10-349-143-320	Sequence 320, App
9	15.8	40.5	50	US-10-131-827-1352	Sequence 1352, App
10	15.8	40.5	50	US-10-131-827-2732	Sequence 2732, App
11	15.8	40.5	50	US-10-131-827-2732	Sequence 2732, App
12	15.8	40.5	51	US-10-287-919-1953	Sequence 1953, App
13	15.8	40.5	60	US-09-894-844-132	Sequence 132, App
14	15.8	40.5	60	US-09-894-844-133	Sequence 133, App
15	15.8	40.5	60	US-09-908-975-13125	Sequence 13125, A

16	15.8	40.5	60	US-10-388-902-132	Sequence 132, App
17	15.8	40.5	25	US-10-388-902-133	Sequence 133, App
18	15.6	40.0	60	US-10-098-263B-19187	Sequence 19187, A
19	15.6	40.0	43	US-10-032-585-1924	Sequence 1924, App
20	15.6	40.0	50	US-10-286-896-23	Sequence 23, Appl
21	15.4	39.5	60	US-09-908-975-11926	Sequence 11926, A
22	15.2	39.0	47	US-10-294-934-1775	Sequence 775, App
23	15	38.5	42	US-09-865-807-21	Sequence 21, Appl
24	15	38.5	42	US-09-954-994A-21	Sequence 21, Appl
25	15	38.5	42	US-09-974-685-21	Sequence 21, Appl
26	15	38.5	42	US-10-187-185-21	Sequence 21, Appl
27	15	38.5	42	US-10-387-304-21	Sequence 21, Appl
28	15	38.5	50	US-10-164-717-13	Sequence 13, Appl
29	15	38.5	60	US-09-908-975-5393	Sequence 5393, App
30	15	38.5	60	US-09-908-975-11986	Sequence 11986, A
31	15	38.5	60	US-09-908-975-12989	Sequence 12989, A
32	15	38.5	60	US-09-908-975-14520	Sequence 14520, A
33	15	38.5	60	US-09-908-975-21363	Sequence 21363, A
34	14.8	37.9	25	US-10-098-263B-35096	Sequence 35096, A
35	14.8	37.9	43	US-10-032-585-806	Sequence 806, App
36	14.8	37.9	43	US-10-032-585-1839	Sequence 1839, App
37	14.8	37.9	47	US-10-294-934-683	Sequence 683, App
38	14.8	37.9	50	US-09-993-346-517	Sequence 517, App
39	14.8	37.9	50	US-10-131-827-3498	Sequence 3498, App
40	14.8	37.9	25	US-09-908-975-17283	Sequence 17283, A
41	14.6	37.4	25	US-10-098-263B-64316	Sequence 64316, A
42	14.6	37.4	33	US-09-828-455-23	Sequence 23, Appl
43	14.6	37.4	33	US-09-828-455-23	Sequence 23, Appl
44	14.6	37.4	47	US-10-349-143-3372	Sequence 3372, App
45	14.6	37.4	50	US-09-993-346-434	Sequence 434, App

ALIGNMENTS

RESULT 1
US-10-131-827-5310
; Sequence 5310, Application US/10131827
; Publication No. US200400094799A1
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9080
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5310
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-131-827-5310

Query Match 49.7%; Score 19.4; DB 15; Length 50;
Best Local Similarity 79.3%; Pred. No. 5e+02;
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 AACCTGAATTTTAAACCGAGTCAA 30
Db 4 AAGTTGAAATTTGCAATCCCAAGTCAA 32

RESULT 2
US-10-349-143-563/c
; Sequence 563, Application US/10349143

```
/ Publication No. US20040005584A1
/ GENERAL INFORMATION:
/ APPLICANT: Cohen, Daniel
/ APPLICANT: Blumenfeld, Marta
/ APPLICANT: Chumakov, Ilya
/ TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
/ FILE REFERENCE: GENSET 020CPI
/ CURRENT APPLICATION NUMBER: US/10/349,143
/ PRIOR FILING DATE: 2003-01-21
/ PRIOR APPLICATION NUMBER: US/09/422,978
/ PRIOR FILING DATE: 1999-10-20
/ PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
/ PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
/ PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
/ PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
/ PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
/ PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
/ NUMBER OF SEQ ID NOS: 11796
/ SEQ ID NO 563
/ LENGTH: 47
/ TYPE: DNA
/ ORGANISM: Homo Sapiens
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 24
/ OTHER INFORMATION: 99-15441-337 : polymorphic base A or C
US-10-349-143-563

Query Match          47.7% Score 18.6; DB 15; Length 47;
Best Local Similarity 68.6%; Pred. No. 1e+03;
Matches 24; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 1 TACTCTGATTTTAAACCCGAAGTCAGAGCT 35
Db 46 TCACATAAAATTTTTCACCTKAGTACATAAGCT 12

RESULT 3
US-10-348-485-30/C
/ Sequence 30, Application US/10348485
/ Publication No. US20030148989A1
/ GENERAL INFORMATION:
/ APPLICANT: Bennett, C. Frank
/ APPLICANT: Dean, Nicholas M.
/ APPLICANT: Holmlund, Jon T.
/ APPLICANT: Dorr, F. Andrew
/ TITLE OF INVENTION: Oligonucleotide Modulation Of Protein Kinase C
/ FILE REFERENCE: ISIS4954
/ CURRENT APPLICATION NUMBER: US/10/348,485
/ CURRENT FILING DATE: 2003-01-21
/ PRIOR APPLICATION NUMBER: US/10/025,139
/ PRIOR FILING DATE: 2001-12-18
/ PRIOR APPLICATION NUMBER: US 08/829,637
/ PRIOR FILING DATE: 1997-03-31
/ PRIOR APPLICATION NUMBER: US 08/478,178
/ PRIOR FILING DATE: 1995-06-07
/ PRIOR APPLICATION NUMBER: US 08/089,996
/ PRIOR FILING DATE: 1993-07-09
/ PRIOR APPLICATION NUMBER: US 07/852,852
/ PRIOR FILING DATE: 1992-03-16
/ NUMBER OF SEQ ID NOS: 121
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 30
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Antisense Oligonucleotide
US-10-348-485-30

Query Match          43.6% Score 17; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 20 CCCGAAGTCAGAGCTA 36
Db 20 CCCGAAGTCAGAGCTA 4

RESULT 4
US-10-131-827-5650/C
/ Sequence 5650, Application US/10131827
/ Publication No. US20040009479A1
/ GENERAL INFORMATION:
/ APPLICANT: Wohlgenuth, Jay
/ APPLICANT: Fly, Kirk
/ APPLICANT: Woodward, Robert
/ APPLICANT: Ly, Ngoc
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
/ FILE REFERENCE: 506612000120
/ CURRENT APPLICATION NUMBER: US/10/131,827
/ CURRENT FILING DATE: 2002-09-06
/ PRIOR APPLICATION NUMBER: US 10/006,290
/ PRIOR FILING DATE: 2001-10-22
/ PRIOR APPLICATION NUMBER: US 60/296,764
/ PRIOR FILING DATE: 2001-06-08
/ NUMBER OF SEQ ID NOS: 9090
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 5650
/ LENGTH: 50
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-131-827-5650

Query Match          43.1% Score 16.8; DB 15; Length 50;
Best Local Similarity 66.7%; Pred. No. 5.2e+03;
Matches 24; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 4 CTCGTGATTTTAAACCCGAAGTCAGAGCTAGTA 39
Db 39 CTCGTGATTTATTCGATCCGAGGCTTAGTGAGGTA 4

RESULT 5
US-10-098-263B-1205
/ Sequence 1205, Application US/10098263B
/ Publication No. US20030104410A1
/ GENERAL INFORMATION:
/ APPLICANT: Miltman, Michael
/ TITLE OF INVENTION: Human Microarray
/ FILE REFERENCE: 3118.1
/ CURRENT APPLICATION NUMBER: US/10/098,263B
/ CURRENT FILING DATE: 2003-01-08
/ PRIOR APPLICATION NUMBER: 60/276,759
/ PRIOR FILING DATE: 2001-03-16
/ NUMBER OF SEQ ID NOS: 131066
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 1205
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-10-098-263B-1205

Query Match          41.0% Score 16; DB 14; Length 25;
Best Local Similarity 79.2%; Pred. No. 9.2e+03;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 14 TTTAAACCCGAAGTCAGAGCTAG 37
Db 2 TTTAAATCCGAAGACACTTCTCG 25

RESULT 6
US-10-333-429-87/C
/ Sequence 87, Application US/10333429
```

```
Publication No. US20040048265A1
GENERAL INFORMATION:
APPLICANT: GENSET
TITLE OF INVENTION: Obesity Associated Biallelic Marker Maps
FILE REFERENCE: G-083US02PCT
CURRENT APPLICATION NUMBER: US/10/333,429
CURRENT FILING DATE: 2003-01-17
PRIOR APPLICATION NUMBER: PCT/IB01/01477
PRIOR FILING DATE: 2001-06-28
PRIOR APPLICATION NUMBER: US 60/219,704
PRIOR FILING DATE: 2000-07-18
NUMBER OF SEQ ID NOS: 579
SOFTWARE: Patent.pm
SEQ ID NO 87
LENGTH: 47
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: allele
LOCATION: 24
OTHER INFORMATION: 99-26989-152 : polymorphic base C or T
US-10-333-429-87
```

```
Query Match 41.0%; Score 16; DB 12; Length 47;
Best Local Similarity 64.7%; Pred. No. 1.1e+04;
Matches 22; Conservative 1; Mismatches 11; Indels 0; Gaps 0;
```

```
QY 6 CTGAAATTTTAAACCCGAGTCAAGCTAGTA 39
DB 47 CAGAAATTTTAAATCAGGTGTCRCATTAAGTA 14
```

```
RESULT 7
US-10-025-367-17/c
Sequence 17, Application US/10025367
Publication No. US20020165186A1
GENERAL INFORMATION:
9118 m2/sr
APPLICANT: Viazxel Biotech GmbH
TITLE OF INVENTION: Compounds that affect CD83 expression, pharmaceutical
FILE REFERENCE: 84201
CURRENT APPLICATION NUMBER: US/10/025,367
CURRENT FILING DATE: 2001-12-19
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patent Ver. 2.1
SEQ ID NO 17
LENGTH: 42
TYPE: DNA
ORGANISM: Homo sapiens
US-10-025-367-17
```

```
Query Match 40.5%; Score 15.8; DB 13; Length 42;
Best Local Similarity 74.1%; Pred. No. 1.2e+04;
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
```

```
QY 4 CTCGAAATTTTAAACCCGAGTCA 30
DB 28 CTCGATTTTCTTAAACCCGGTTAAA 2
```

```
RESULT 8
US-10-349-143-320
Sequence 320, Application US/10349143
Publication No. US20040005584A1
GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marra
APPLICANT: Chumakov, Ilya
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
FILE REFERENCE: GENSET.020CPI
CURRENT APPLICATION NUMBER: US/10/349,143
```

```
CURRENT FILING DATE: 2003-01-21
PRIOR APPLICATION NUMBER: US/09/422,978
PRIOR FILING DATE: 1999-10-20
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796
SEQ ID NO 320
LENGTH: 47
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: allele
LOCATION: 24
OTHER INFORMATION: 99-14204-468 : polymorphic base G or T
US-10-349-143-320
```

```
Query Match 40.5%; Score 15.8; DB 15; Length 47;
Best Local Similarity 69.0%; Pred. No. 1.3e+04;
Matches 20; Conservative 1; Mismatches 8; Indels 0; Gaps 0;
```

```
QY 1 TAACTGAAATTTTAAACCCGAGTCA 29
DB 13 TAACTTAAATKTTTAAAGATGAGTAA 41
```

```
RESULT 9
US-10-131-827-1352
Sequence 1352, Application US/10131827
Publication No. US20040009479A1
GENERAL INFORMATION:
APPLICANT: Wohlgenuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
FILE REFERENCE: 506612000120
CURRENT APPLICATION NUMBER: US/10/131,827
CURRENT FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: US 10/006,290
PRIOR FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: US 60/296,764
PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 9090
SOFTWARE: Patent version 3.1
SEQ ID NO 1352
LENGTH: 50
TYPE: DNA
ORGANISM: Homo sapiens
US-10-131-827-1352
```

```
Query Match 40.5%; Score 15.8; DB 15; Length 50;
Best Local Similarity 65.7%; Pred. No. 1.3e+04;
Matches 23; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
```

```
QY 2 AACTGAAATTTTAAACCCGAGTCAAGTCA 36
DB 8 AACTGAAATTTTGAAACGAGTATTGAGAGACTA 42
```

```
RESULT 10
US-10-131-827-2732/c
Sequence 2732, Application US/10131827
Publication No. US20040009479A1
GENERAL INFORMATION:
APPLICANT: Wohlgenuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc
```

```

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; PRIOR FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 2732
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-2732

Query Match          40.5%; Score 15.8; DB 15; Length 50;
Best Local Similarity 65.7%; Pred. No. 1.3e+04;
Matches 23; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 TAACCTGAAATTTTAAACCCGAAGTCAGAGCT 35
DB 43 TATGTATTATTTTGAACCGATGCTCAGAGTT 9

RESULT 11
US-10-131-827-4948
; Sequence 4948, Application US/10131827
; Publication No. US20040009479A1
; GENERAL INFORMATION:
; APPLICANT: Wollgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 4948
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-4948

Query Match          40.5%; Score 15.8; DB 15; Length 50;
Best Local Similarity 65.7%; Pred. No. 1.3e+04;
Matches 23; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 2 AACTCTGAATTTTAAACCCGAAGTCAGAGCTA 36
DB 8 AAATCTGATTTTGGAAACGAGTATTGGAGGACTA 42

RESULT 12
US-10-287-919-1953/c
; Sequence 1953, Application US/10287919
; Publication No. US20030085830A1
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Methanococcus jannaschii complete genome.
; FILE REFERENCE: Jim Zeegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/287,919
; PRIOR FILING DATE: 2002-11-05
; NUMBER OF SEQ ID NOS: 2706
; SOFTWARE: Proprietary
```

```

; SEQ ID NO 1953
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Methanococcus jannaschii complete genome.
; FEATURE:
; LOCATION: (1161190)...(1161241)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectionObjectNumber = 2488
US-10-287-919-1953

Query Match          40.5%; Score 15.8; DB 14; Length 51;
Best Local Similarity 89.5%; Pred. No. 1.3e+04;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AACTCTGAATTTTAAAC 20
DB 32 AATCTGATTTTAAAC 14

RESULT 13
US-09-894-844-132
; Sequence 132, Application US/09894844
; Patent No. US20020176873A1
; GENERAL INFORMATION:
; APPLICANT: Behr, Marcel
; APPLICANT: Small, Peter
; APPLICANT: Schoolnik, Gary
; APPLICANT: Wilson, Michael A.
; TITLE OF INVENTION: Molecular Differences Between Species of
; FILE REFERENCE: STAN102CON
; CURRENT APPLICATION NUMBER: US/09/894,844
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 09/318,191
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 60/097,936
; PRIOR FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 132
; LENGTH: 60
; TYPE: DNA
; ORGANISM: M. tuberculosis
US-09-894-844-132

Query Match          40.5%; Score 15.8; DB 9; Length 60;
Best Local Similarity 74.1%; Pred. No. 1.4e+04;
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2 AACTCTGAATTTTAAACCCGAAGTC 28
DB 19 AATTGTGAATTCATCAACCGCTAGTC 45

RESULT 14
US-09-894-844-133
; Sequence 133, Application US/09894844
; Patent No. US20020176873A1
; GENERAL INFORMATION:
; APPLICANT: Behr, Marcel
; APPLICANT: Small, Peter
; APPLICANT: Schoolnik, Gary
; APPLICANT: Wilson, Michael A.
; TITLE OF INVENTION: Molecular Differences Between Species of
; FILE REFERENCE: STAN102CON
; CURRENT APPLICATION NUMBER: US/09/894,844
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 09/318,191
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 60/097,936
; PRIOR FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: FastSeq for Windows Version 4.0
```

; SEQ ID NO 133
; LENGTH: 60
; TYPE: DNA
; ORGANISM: M. tuberculosis
US-09-894-844-133

Query Match 40.5%; Score 15.8; DB 9; Length 60;
Best Local Similarity 74.1%; Pred. No. 1.4e+04;
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2 AACTCTGAATTTTAAACCCGAGTC 28
Db 19 AATTGTGAATTCATACAGCCGTAGTC 45

RESULT 15
US-09-908-975-13125
; Sequence 13125, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Eli
; APPLICANT: FAIGLER, Simcha
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLIC
; TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13125
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-13125

Query Match 40.5%; Score 15.8; DB 10; Length 60;
Best Local Similarity 65.7%; Pred. No. 1.4e+04;
Matches 23; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 2 AACTCTGAATTTTAAACCCGAGTCAGAGCTA 36
Db 11 AACTCTGCTTAGAAGAAACATGACACAGGGGCAA 45

Search completed: March 20, 2004, 11:47:36
JOB Time : 197 secs